# Mobile genetic elements Methanobacterium thermoformicicum



40551

# BIBLIOTHEEK CANDBOUWUNIVERSITER WAGENINGEN

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Mobile genetic elements in Methanobacterium thermoformicicum

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van de Landbouwuniversiteit te Wageningen



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#### Stellingen

- Gezien het grote aantal niet-gekarakteriseerde prokaryoten lijkt de indeling in Archaea en Bacteria door C. R. Woese en medewerkers van voorlopige aard.
   Woese et al. 1990, Proc. Natl. Acad. Sci. USA 287:4576-4579
- Het niet in aanmerking nemen van DNA-modifikaties kan bij het in kaart brengen van prokaryotische genomen het trekken van verkeerde conclusies bevorderen.
   R. Stettler en T. Leisinger (1992). J. Bacteriol. 174:7227-7234.
- 3. De isolatie van thermofiele methanogenen uit riviersedimenten impliceert dat deze organismen wellicht beter als 'fakultatieve thermofielen' beschreven kunnen worden.

Dit proefschrift, Hoofdstuk 2

- 4. Onverwachte resultaten zijn de meest interessante.
- 5. Vooroordelen tegenover vluchtelingen berusten op vluchtige indrukken.

  Amnesty International
- 6. Het aanwakkeren van een oorlogsstemming door nederlandse media tijdens bepaalde internationale voetbalwedstrijden is onaanvaardbaar.
- Het valt moeilijk te verklaren dat experimentjes met plasmiedjes en faagjes soms leuker kunnen zijn dan rustigjes met een krantje en een pilsje in het zonnetje te zitten.
- 8. Verkorting van de studieduur bevordert niet de noodzakelijke 'cultuuroverdracht' (*de Volkskrant*, 09.01.93) aan de universiteit maar versterkt de trend tot opleiding van vakspecialisten met geïsoleerde kennis.
- 9. De aanpak van milieuproblemen wordt belemmerd omdat met onaangename waarheden geen verkiezingen te winnen zijn.
- 10. Het is aan te bevelen om met het formuleren van stellingen op tijd te beginnen.

Stellingen behorende bij het proefschrift "Mobile genetic elements in Methanobacterium thermoformicicum" van Jörk Nölling.

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#### General introduction

The diversity of life as the result of evolution from a common origin has generated considerable interest in the classification of organisms. The accuracy, however, with which a phylogenetic tree reflects the relationships among the organisms strongly depends on the markers and methods used for comparison. In general, markers that are directly related to the nucleotide sequences of a genome are more informative for the determination of phylogenetic relationships than are phenotypic properties (157). A nevertheless meaningful phenotypic classification was the division of the living world into the major groups of prokaryotes and eukaryotes which initially was based on readily detectable phenotypic properties such as the pronounced differences in their cellular organization. Only later this distinction was confirmed by the identification of comparable molecular characteristics such as differences in ribosome structure (159). However, the prokaryote-eukaryote dichotomy was based on the comparison of eukaryotic markers with those derived from the model bacterium *Escherichia coli* that was considered as a typical representative of the prokaryotic kingdom (159).

Compared to the phenotypic diversity of eukaryotes, the prokaryotes constitute a group of phenotypically relatively homogeneous organisms. This led to the assumption that the prokaryotes have a monophyletic origin, i.e. are descendants of a single common ancestor. Despite the lack of complex phenotypic markers, prokaryotic systematics was mainly based on comparative morphology of cells or colonies, differences in cell-walls revealed by Gramstaining and readily detectable physiological properties such as growth with or without oxygen, nitrogen fixation or photosynthesis (157). However, those criteria have only limited value for prokaryotic taxonomy mainly for two reasons (157). Firstly, lateral gene transfer or adaptation to environmental stress may have resulted in similar phenotypes of two distantly related organisms. And secondly, the evaluation of a phenotypic marker as phylogenetically significant is often a subjective one (157).

More reliable information on the prokaryotic phylogeny was obtained from analysis of various molecular markers. Cell wall analysis and immunological studies, together with initial approaches in genotype-based classification such as comparison of the DNA base ratios (GCcontent) and analysis of the total DNA relatedness, were applied in the phylogenetic characterization of lower taxa (157). A considerable step forward was the use of macromolecules as 'evolutionary clocks' to determine evolutionary distances (72). Macromolecules such as nucleic acids and proteins consist of a large number of independent constituents, i.e. nucleotides and amino acids, whose sequential order provides the information for their function. Since the number of possible different sequences is extremely high, two sequences with extensive similarity are most likely evolutionary related rather than the product of convergent evolution. As the result of continuously occurring, selectively neutral mutations, the observed accumulated differences between two sequences are analogous to a relative time span, i.e. the sequence differences can be used to calculate the evolutionary distance of the compared sequences from a common ancestor. Among the sequences that may be used as molecular chronometers for phylogenetic analysis of higher taxa, most suitable ones are those that have been established in early stages of cell's evolution. Among those, ribosomal RNAs are extremely suitable since (i) they are functionally highly constant and universally distributed, (ii) they contain enough information to be statistically reliable, (iii) they contain both moderately and highly conserved regions and, therefore, are suitable for measuring both small and large phylogenetic distances, and finally (iv) their isolation and analysis is relatively easy (159).

Based on comparative analysis of 16S rRNA sequences, Woese and coworkers discovered a basic division of the known prokaryotic organisms that led them to propose a third primary lineage distinct from eubacteria and eukaryotes, designated archaebacteria (Figure 1). A similar classification was established by comparison of other molecular chronometers with the capacity for high-taxa-resolution such as for instance components of the DNA-dependent RNA polymerase (74, 174), translation factors (20, 47) and ATPase components (37, 60, 62). Certain group-specific features could be identified on the molecular genetic and biochemical level (for review: 173) which confirmed the distinction between the three 'urkingdoms' of life. Since the new, genotype-based taxonomy should be reflected in terminology, Woese and coworkers (1990) proposed to rename the three primary lineages into the 'domains' Archaea, Bacteria and Eucarya (Figure 1).

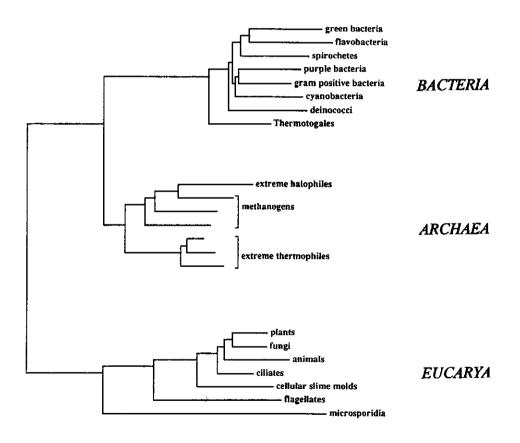


Figure 1. Unrooted universal phylogenetic tree (taken from Woese [159]), based upon 16S rRNA sequence comparison, showing the known three domains of life.

Besides certain unique archaeal characteristics as ether-linked lipids (26), unusual modified tRNA-nucleotides (30) and the methanogenic C<sub>1</sub>-metabolism (27, 68), most of the features that allow to distinguish the Archaea from the Bacteria and the Eucarya are associated with the genetic machinery (173). The archaeal genomes appear to be composed of a single circular chromosome similar to the genome of their bacterial counterparts. As in Bacteria, archaeal genes are - with the exception of certain genes from halophilic organisms (10) preceded by Shine-Dalgarno sequences and frequently are organized in transcriptional units (10). The majority of the archaeal features, however, were found to be more similar to those from the Eucarya such as the presence of introns (73, 111) and 7S RNA (66), the structure of promoters (44, 48), and the sensitivity to certain antibiotics (165, 173). This striking similarity between Archaea and Eucarya is also reflected by sequence comparison of ribosomal proteins (156), translation factors (20, 47), components of the DNA-dependent RNA polymerase (74, 173), DNA ligases (75), components of the ATPase (37, 60, 62) and histone-like proteins (129). Although not reflected on 16S RNA-level, this archaeal-eucaryal similarity in basic molecular characteristics provides reasonable arguments for a closer relationship of the Archaea to the Eucarya than to the Bacteria. In contrast, the sequences of enzymes of the central metabolism as GAPDH (50), malate dehydrogenase (57), 3phosphoglycerate kinase (33) and  $\beta$ -glucosides hydrolyzing enzymes (31) were found to be more related between Bacteria and Eucarya (173).

The domain Archaea comprises at least three major groups of prokaryotic organisms with, compared to their bacterial counterparts, unusual phenotypes: the extreme thermophilic, sulfur-dependent species, the extreme halophiles and the methanogens (159). Phylogenetically, the Archaea can be subdivided into two main lineages (kingdoms): the Crenarchaeota (158) which comprise most of the hyperthermophiles, and the Euryarchaeota (158), a phenotypically more diverse collection of organisms including the three groups of methanogens, the extreme halophiles, the extreme thermophilic genera Thermococcus and Thermoplasma and the sulfate-reducing Archaeoglobus. The branching order of the euryarchaeotal tree suggests that this kingdom has evolved from an ancient sulfur-reducing, hyperthermophilic organism via the methanogenic to the extreme halophilic organisms (159). Moreover, it is assumed that an extreme thermophilic, sulfate-reducing organism has been the common ancestor of the Archaea since this phenotype is the only one shared by both archaeal kingdoms (158).

Methanogens are, with respect to morphology and growth requirements, a diverse group which obtain their energy for growth from the conversion of low molecular weight compounds to methane (for review: 154). The main products of fermentative decomposition of organic matter,  $H_2$  and  $CO_2$ , formate, and acetate are the major substrates of methanogenic bacteria. In addition, other  $C_1$ -compounds and certain alcohols may serve as substrates. Methanogens exist as free-living and endosymbiotic organisms (150) and occupy a wide range of anaerobic habitats in soil and aquatic environments, the intestines of certain organisms, bioreactors, and extreme environments such as hydrothermal vents and hypersaline lakes.

The biotechnological importance of methanogenic bacteria is reflected by their application in biodegradation of waste and the simultaneous production of biogas as an alternative form of energy and their potential to convert xenobiotics (2, 19, 53, 77). In addition to these (potential) applications, the scientific interest in molecular biology of methanogenic bacteria as representatives of the *Archaea* accounts for the progress in the genetics of methanogens which was subject of various recent reviews (10, 122, 171).

#### MOBILE GENETIC ELEMENTS

Prokaryotic chromosomes are regarded to consist of a set of essential genes which are interspersed with a variety of sequences including accessory genes, noncoding segments and (short) repeated sequences (80). Retaining a basic stability of the genomic organization, the chromosomal DNA is subjected to several genetic changes including point mutations and small and large scale rearrangements such as insertions, deletions and inversions. In addition to those changes of the resident genetic material, horizontal gene transfer serves as an important source for genomic variations which allow an adaptation of the host to environmental stress conditions. As a consequence of the uptake and assimilation of foreign DNA, the chromosome can be viewed as a mosaic, comprising recipient-derived DNA interspersed with DNA from other sources (141).

A comparable organization and dynamic nature as found for the chromosomal DNA is in principle also found in the smaller-sized genomes of plasmids and phages. Therefore, elucidation of the genomic organization of these elements may provide insight into the structure of genomes in general. Moreover, plasmids and phages belong, together with insertion sequences (IS), to a class of accessory elements that force the change of the cell's genomic constitution: their movement within or between prokaryotic genomes often is accompanied with genomic rearrangements (promoted by insertion elements) and the horizontal transmission of genetic material (plasmid- and phage-mediated). Thus plasmids, phages and insertion elements which together constitute a family of mobile genetic elements (79), appear to play a significant role in evolutionary processes.

The naturally occurring IS elements comprise defined DNA sequences ranging from 0.8 to 3 kb and are joined to autonomously replicating molecules (replicons) such as the prokaryotic chromosome, phage- and plasmid DNA. A characteristic of these mobile elements is that they specify functions that allow them to move from one site to another, either intra- or intermolecularly. Different types of genomic changes are promoted by IS elements (35): (i) transposition of IS elements itself may cause disruption of coding regions or may lead to a fusion of replicon, (ii) the presence of several genomic copies of IS elements provide sites for reciprocal recombination which results in genomic rearrangements such as deletions and inversions, and (iii) two IS elements flanking genomic-derived genes may form a composite transposon thereby mobilizing the internal genomic sequences.

Plasmids and phage genomes are, in contrast to IS elements, autonomously replicating genetic elements that either exist extrachromosomally or - as the result of site-specific integration or homologous recombination - may become part of the host chromosome. While the mobility of IS elements is restricted to the genome of a single cell, many plasmids and phages have the potential to mediate the transfer of their genomes from one cell to another. This transmission of DNA can be accompanied by mobilization of host DNA, including IS elements, by conjugation (plasmid-directed) and transduction (phage-directed). In addition to natural transformation, i.e. the uptake and incorporation of exogenous DNA, conjugation is regarded as the major mechanism for horizontal DNA transfer in nature that occurs between phylogenetically divergent prokaryotes (1, 87) and may even bridge the boundaries between members of different domains, including DNA transfer between pro- and eukaryotes (interkingdom sex') (1, 49, 141).

The study of genetic mobile elements may therefore contribute to the understanding of genomic organization and processes that influence the genetic constitution of prokaryotic organisms. Moreover, in particular plasmids are useful model systems for the investigation of the fundamental process of DNA replication and may serve as basic tools in recombinant

DNA technology.

#### ARCHAEAL MOBILE ELEMENTS

#### **Plasmids**

Plasmids have been identified in all three major groups of Archaea (for review: 10; Table 1).

Among the hyperthermophilic, sulfur-dependent Archaea only two plasmids, designated pGT5 (32) and pBG from Sulfolobus strain B6 (143), have been described whereas two other extrachromosomal elements, pSB12 and pSL10, represent lysogenic forms of viruses or virus-like particles that will be discussed in the next section. The small, 3.45-kb multicopy plasmid pGT5 is harbored by a recently isolated hyperthermophilic archaeon (strain GE5) which has an optimal growth temperature of 94°C (32). Surprisingly, pGT5 was found to be nearly relaxed at physiological temperatures (95°C) (11), although strain GE5 contains reverse gyrase activity that is common to extreme thermophilic organisms of both archaeal and bacterial origin (8, 9). This activity was believed to be necessary for thermostabilization of closed circular DNA by introduction of positive supercoils. It is supposed that the relaxed state of pGT5 at physiological temperatures in vivo is the result of both reverse gyrase activity and the presence of nucleosome-like structures and might be representative for the topology of chromosomal and extrachromosomal DNA of hyperthermophiles (11, 34).

Most progress in biology of archaeal plasmids has been made with those from the extreme halophilic organisms. For a part this is due to the large number of plasmids that have been described for these organisms, ranging in size from small, 1.7-kb high copy number plasmids up to 690-kb megaplasmids (Table 1), and the established transformation systems (see below). Many halophilic bacteria contain heterogeneous plasmid populations and a considerable part of the genomic information is located on extrachromosomal elements (14, 40, 112, 127, 145). The 150-kb pHH1 has been identified as the main plasmid of Halobacterium halobium (153) (several strains of H.halobium and H.cutirubrum probably belong to the species H.salinarium according to Tindall [1992]). Plasmid pHH1 contains a large number of different halobacterial IS elements that cause insertion, deletions and rearrangements of pHH1 (115, 118, 119). Other Halobacterium species were found to contain structural derivatives of pHH1, either as covalently closed DNAs or integrated into the chromosome (28, 112). Initial observations of an correlation between the ability to form gas vesicle and the presence of plasmids (137, 153) has led to the identification of vac genes located on the plasmids pHH1 (58) and pNRC100 (23, 64). Detailed analysis of the 200-kb pNRC100 resulted in the identification of two large (35 to 38 kb) inverted sequences which are supposed to mediate inversion of the intervening single-copy regions, one of which contains the vac-region, and constitute a possible regulation mechanism for gene expression (100). In addition, the origin of replication has been mapped for plasmid pNRC100 (100), pHH1 (119) and pHK2 (56). A function could also assigned to plasmid pΦHL, a deletion derivative of the  $\Phi$ H prophage (133) whose nucleotide sequence and transcriptionally active regions have recently been determined (38). H.halobium R<sub>1</sub> cells carrying pΦHL become resistant to infection by phage  $\Phi H$  due to a immunity-conferring coliphage-like repressor encoded by  $p\Phi HL$  (69).

Treatment of H.halobium GRB with the gyrase inhibitor novobiocin resulted in the

Table 1. Archaeal plasmids

Plasmid	Host  Sulfolobus strain B6	Size (kb)	References for Relevant Characteristics					
		(kU)	Isolation/Seque	nce Function <sup>b</sup>	Transformation			
pBG <sup>d</sup>		35	(143)	_	_			
pGT5	hyperthermophilic, sulfur-metabolizing isolate GE5	3.5	(32)	-	-			
pNRC100	Halobacterium halobium NRC-1°	200	(23)	vac genes (23, 64)	_			
pHH1	H.halobium NRC817	143	(153)	vac genes (58)	(6, 18)			
pHH2	H.halobium DSM670	152	(11 <b>2</b> )	_	_			
рНН3	H.halobium DSM671	76	(112)	-	_			
pHSB1	H.halobium SB3	1.7	(28/41)	Rep protein (61)	(41, 85)			
pHGN1	H.halobium GN101	1.8	(28/45)	Rep protein (61)	_			
pGRB1	H.halobium GRB	1.8	(28/42)	Rep protein (61)	(17)			
₽ <b>₽</b> HL	H.halobium R <sub>I</sub> L	19	(133/38)	ΦH immunity (133, 6	9) –			
pHT1	H.trapanicum	122	(112)	-	-			
pHT2	H.trapanicum	6	(112)	-	-			
pHC1	H. cutirubrum	122	(112)	_	_			
pΒ	Halobacterium salinarium 5	41	(136)	_	_			
pRDS102	H.salinarium 5	69	(136)	vac genes (136, 137	) -			
pD	H.salinarium 5	134	(136)	_	-			
pHV1	Haloferax volcanii DS2	86	(112)	_	_			
pHV2	H.volcanii DS2	6.4	(112/12)	-	(12, 84, 101)			
pHV3	H.volcanii DS2	440	(14)	_	_			
pHV4	H.volcanii DS2	690	(14)	_	_			
pHV11	H.volcanii WR11	13	(126)	_	_			
pHV12	H.volcanii WR12	25	(126)	_	-			
pHV13	H.volcanii WR13	44	(126)	-	_			
pHK2	Haloferax Aa2.2	10.5	(54)	-	(54, 56, 84, 101)			
pHM1	Halococcus morrhuae CCM 537	48	(96)	_	_			
pHM2	H.morrhuae CCM 537	6	(96)	-	-			
pC2A	Methanosarcina acetivorans C2A	5.1	(140)	-	_			
pURB500	Methanococcus sp. nov.	8.7	(160)	_	-			
pURB800	Methanococcus jannaschii	64	(166)	-	_			
p <b>URB80</b> 1	M. jannaschii	18	(166)	-	-			
p <b>URB90</b> 0	Methanococcus AG86	20	(166)	-	-			
pMP1ª	Methanolobus vulcani	6.9	(144, 155)	-	-			
pT3	Methanobacterium sp. nov.	7.3	(5)	-	_			
pME2001	M.thermoautotrophicum Marburg	4.4	(88/7)	-	_			
pFV1	M.thermoformicicum THF	13.5	(103/106)	MthTI system (104)	· –			
pFZ1	M.thermoformicicum Z-245	11	(103/106)	MthZI system (105)	· –			
pFZ2	M.thermoformicicum FTF	11	(103)	MthFI system (105)	_			

Complete nucleotide sequence.

b Identified functions (based on experimental data or on homology with known proteins), including plasmid replicationand maintenance functions.

Transformation of the natural host or close relatives using the original plasmid or engineered derivatives including shuttle vectors.

d Possibly represents a prophage.

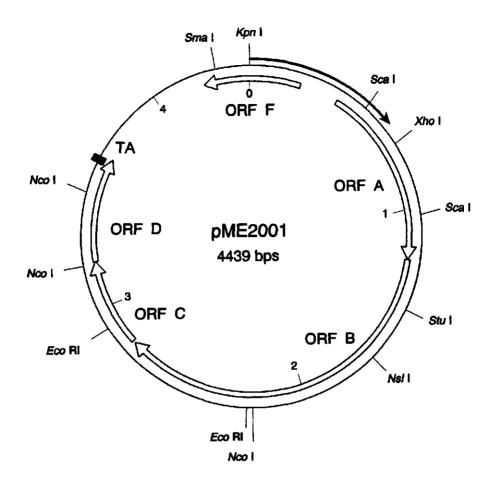
<sup>\*</sup> Several strains of H.halobium and H.cutirubrum belong to the species H.salinarium (146).

accumulation of single stranded forms of the small 1.8-kb multicopy number plasmid pGRB1 suggesting that this plasmid replicates via a rolling circle mechanism (39, 139). Since sequence analysis of pGRB1 and the similar sized plasmids pHSB1 and pHGN1 revealed that each plasmids could code for a homologous protein of approximately 35 kDa (41, 42, 45), these putative proteins may be involved in a common mode of plasmid replication (42). This hypothesis was recently supported by Ilyina and Koonin (61), who found that the plasmid-encoded proteins of pGRB1, pHSB1 and pHGN1 share a conserved sequence motif with rolling circle replication initiation proteins.

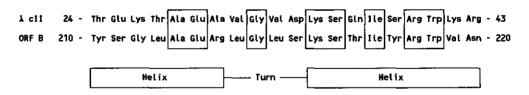
The application of genetic engineering techniques in halophilic members of the archaeal domain became possible with the development of efficient transformation systems. A natural mating system (94, 125) and a protoplast fusion technique (126) have been described for Haloferax volcanii. The polyethylene glycol mediated spheroplast transformation method, however, is the most commonly applied one and transformation protocols have been developed for the phylogenetically distant H.halobium (15, 41), H.volcanii (12, 17) and members of the genus Haloarcula (18). The vector plasmids used for transformation studies were derivatives of small halobacterial replicons equipped with a marker gene and, more recently, were expanded to halobacterial-E.coli shuttles vectors (6, 56, 84, 85). Selective markers used included genes conferring resistance to novobiocin (54) or mevinolin (84), or encoding a phenotypically selectable marker, such as gas vesicle synthesis (6). Expression of the bacterio-opsin (bop) gene in a bop mutant of H.halobium was observed after transformation with a pGRB1-based multicopy vector that carried an intact bop gene (82). Using a mutated halobacterial gyrase B gene which confers resistance to novobiocin (55) as selective marker, a cloning vector was constructed based on the pHK2 replicon of Haloferax Aa2.2 (54). Subcloning into an E.coli vector yielded the shuttle-vector pMDS1 which, however, could only stably maintained in Haloferax if propagated in a dam E.coli strain since methylated adenine residues are subject to restriction in the halophilic host (56). A derivative of pMDS1 has recently been used for expression of a alkaline serine protease, termed halolysin, from an unidentified halophilic strain in H. volcanii (67). Two other halobacterium-E.coli shuttle vectors, pUBP2 (derived from pHH1 of H.halobium; 6) and pWL102 (based on the H. volcanii pHV2 replicon; 84) were found to stably transform members of different halophilic genera (18) and may be useful as generalized cloning vectors in halophilic Archaea. The pHV2-derived vector has been used in complementation experiments to analyze the minimal DNA region necessary for gas vesicle synthesis (59). Recently, transformation of H.halobium was applied for specific in vivo rRNA mutagenesis of its single-copy rRNA operon (85). This technique makes use of a shuttle vector pHRZH, a derivative of pHSB1 from H.halobium SB3 (28) which is equipped with a mutated, H.halobium rRNA operon that confers resistance to two different antibiotics. After transformation, the sensitive, single-copy wild-type rRNA operon of the recipient is replaced by the vector-borne one via recombination, resulting in a transformed strain that directs synthesis of exclusively mutated ribosomes (85).

Representatives of all three major lines of the methanogenic branch of the Archaea were found to harbor plasmids (Table 1) ranging in size from 4.4 kb for the high-copy number plasmid pME2001 from Methanobacterium thermoautotrophicum Marburg (88) up to 64 kb for pURB800 from Methanococcus jannaschii (166). However, compared to what is known about plasmids from halophilic bacteria, only little progress has been made in plasmid biology of methanogens. This may be attributed to the fact that, compared to the halophilic Archaea, (i) plasmids are less common among methanogens, (ii) all plasmids identified so

A



В



C

 $\lambda$  cII ( $P_{RE}$ ) GCCTCG<u>TTGC</u>GTTTGT<u>TTGC</u>ACGAAC

TA1 3616 - TITATT<u>TTGA</u>TTTTTT<u>TAGA</u>TTTTTT<u>TAGA</u>TTTTTTTCTATC - 3575

TA2 3685 - ATTITCTTGTATTTTTTTTCCTTCA - 3659

TA3 3771 - TTTTAT<u>TTGC</u>ATTTT<u>TTGC</u>ATTTTC<u>TTGT</u>ATTTT<u>TTGC</u>TTTCTCA - 3725

Figure 2. (A) Physical map and coding regions of plasmid pME2001 of *M.thermoautotrophicum* Marburg. ORFs A through F are indicated by open arrows whereas the mapped 611-bp transcript (91) is shown as a black arrow. The putative ORF B protein binding region (TA) is denoted by a solid block. Sizes are given in kilobases. (B) Comparison of the helix-turn-helix motif of the  $\lambda$  cII activator protein (51) with that deduced from ORF B. Identical amino acids are boxed. Numbers refer to the amino acid position. (C) Binding site of the  $\lambda$  cII protein (51) compared to the putative ORF B protein binding region of pME2001 (TA) composed of three sequence stretches (TA1 through TA3). Tetranucleotides similar to TTGC and spaced by six nucleotides are underlined. Numbers refer to sequence position according to Bokranz et al. (7).

far in methanogens are cryptic, i.e., no phenotype could be correlated with the presence of plasmids, and (iii) an efficient transformation system and suitable vectors are at present not available.

One of the best studied plasmids is pME2001 of M. thermoautotrophicum Marburg. This plasmid which is present in about 20 copies per host chromosome (102), turned out to be very stable since several attempts failed to cure strain Marburg from pME2001 (102). The dispensability of pME2001 was, however, demonstrated by Leisinger and coworkers who reported the isolation of a pME2001-free derivative of strain Marburg after treatment with the mutagen N-methyl-N'-nitro-nitrosoguanidine (70, 92). The nucleotide sequence of pME2001 comprises 4439 bp (7) and contains six open reading frames, designated ORF A through ORF F, which could code for proteins composed of more than 100 amino acids (Figure 2A). Except for ORF C, all ORFs are preceded by a potential ribosome binding site (10). The head-to-tail-organization of ORF A-D may suggest a coordinate transcription and translation of the four ORFs. Although no sequences with significant similarity to the boxA/boxB motif of an archaeal consensus promoter signal (44, 48) could be localized upstream from ORF A, the identification of a 611-bp-transcript of pME2001 by Meile and coworkers (91) which covers the potential promoter regions of the ORF A and ORF F. respectively (Figure 2A), may support cotranscription of ORF A-D. The small size of the transcript may be explained as the result of posttranscriptional processing or nucleolytic degradation of a primary transcript (91). A sequence stretch with excellent similarity to the archaeal consensus promoter signal is located approximately 170 bp upstream of ORF F. Possibly, the expression of the ORF F protein is regulated since translation of the ORF F mRNA might be blocked by the mapped 611-bp-RNA which is transcribed from the opposite DNA-strand and would therefore serve as anti-sense RNA (Figure 2A).

No significant similarity was found between the deduced proteins of pME2001 and proteins stored in the database. Screening of the pME2001 proteins for the presence of certain amino acids motifs has shown, however, that the ORF B protein contains a helix-turn-helix (HTH) motif which might enable the ORF B protein to bind to DNA (Nölling, unpublished results). Moreover, the HTH motif of the ORF B protein was found to be similar with the HTH motif of the transcription activator cII from phage  $\lambda$  (51). The identical residues shared by both HTH motifs were in particular located at those positions of the  $\lambda$  cII protein that are believed to be involved in recognition of a specific DNA sequence (51) (Figure 2B). This may suggest that the ORF B protein recognizes the same DNA target as the  $\lambda$  cII transcription activator, i.e. two TTGC tetranucleotides repeats spaced by six nucleotides: TTGC-N<sub>6</sub>-TTGC (51). We could identify a region located at the 3'-end of ORF D of plasmid pME2001 that showed homology to the  $\lambda$  cII target-sequence. This pME2001-region, designated TA-region, is 193

bp in size and contains three sequence stretches (TA1-TA3) with the same or similar tetranucleotide repeats separated by six nucleotides as found for the  $\lambda$  cII-target (Figure 2C). An additional remarkable feature of TA1-TA3 sequences is the fact that those tetranucleotide repeats in turn separate several runs of four to six thymidine nucleotides which may induce bending of the DNA (78) (Figure 2C). Such bent DNA regions are known to be important for various molecular-biological processes such as for instance replication and transcription (43). It seems therefore possible that the putative DNA binding ORF B protein and the TA-region play a role in replication of plasmid pME2001.

Several pME2001-based vectors have been constructed that may be used for replication in *Bacteria* and *Eucarya* (89, 90). However, besides a low-level natural transformation system for *M.thermoautotrophicum* Marburg (162), no efficient reintroduction of DNA into this methanogenic host has been reported so far. The development of a transformation system is therefore the bottle neck for examination of *in vitro* modified DNA in *Methanobacterium* strains.

Promising results in establishing a transformation have been reported for the mesophilic Methanococcus voltae PS. Based on its low-level natural competence (4), transformation of this organism with a vector that was able to integrate in the chromosome of the recipient, was demonstrated by Gernhardt and coworkers (36). The integration vector used was equipped with an expression cassette comprising the puc gene from Streptomyces alboniger (83) as selective marker which conferred puromycin resistance to its methanogenic host. Similar results were obtained with Methanococcus maripaludis used as recipient (128). Increased transformation rates of auxotrophic M. voltae PS with wild type chromosomal DNA could be achieved by electroporation as alternative transformation method (95). These results suggest that an efficient host-vector system for Methanococcus could be based on an improved electroporation protocol in combination with an autonomously replicating vector that carries the puromycin-resistance cassette (36) as selective marker. The vector may be derived from a plasmid of a related species, such as pURB500 isolated from a marine Methanococcus species (160).

#### Viruses and Virus-like Particles

Similar as representatives of the eucaryal and bacterial domain also those belonging to the archaeal domain are subject to viral infection. Table 2 lists the viruses and virus-like particles (VPLs: nucleic acid containing particles whose infectivity have not been proven) that have been described for representatives of the three major lineages of the archaeal domain, the extreme thermophilic, sulfur-dependent, the extreme halophilic and the methanogenic Archaea (for review: 172). All archaeal viruses and VLPs, isolated so far, contain a double-stranded DNA genome although this does not exclude the possibility of the existence of archaeal viruses with single-stranded DNA or RNA genomes. With the exception of the VLP isolated from Methanococcus voltae A3 (161), viruses of the extreme halophilic and methanogenic branch were similar in morphology to those of the bacterial domain composed of a polyhedral head and a tail. By contrast, unusual lemon- or rod-shaped virus structures are common to the viruses and VPLs that infect extreme thermophilic, sulfur-dependent Archaea. In addition, the genomes of the latter viruses and VLPs are only small in size compared to those found for the viruses of halophiles and methanogens (Table 2).

The temperate virus SSV1 (formerly SAV1) of the extremely thermophilic, sulfur-

Table 2. Archaeal viruses and virus-like particles

Name	Host	Virion morphology	DNA topology	Genome size (kb)	Туре	References
SSV1	Sulfolobus solfataricus	lemon	ccca	15.5	temperate	(86, 109, 130, 168)
VPL-B6b	Sulfolobus sp. B6	polyhedric	n.d.°	n.d.	temperate	(172)
DAV 1 <sup>d</sup>	Desulfurococcus ambivalens	lemon	ccc	7.7	temperate	(167, 168, 172)
CWP	Pyrococcus woesei	polyhedric	n.d.	n.d.	n.d.	(170, 172)
TTV1	Thermoproteus tenax Kral	rod	linear	15.9	temperate	(63, 98, 172)
TTV2	T.tenax Kral	flexible rod	linear	16	temperate	(63, 172)
TTV3	T.tenax Kra1	flexible rod	linear	27	n.d.	(63, 172)
TTV3	T.tenax Kral	rod	linear	17	lytic	(63, 172)
₽H	Halobacterium halobium	complex <sup>g</sup>	linear	59	temperate	(38, 131, 135, 172)
ΦN	H.halobium	complex	linear	56	temperate	(151)
Hs1 HsL	H. salinarium	complex	linear	n.d.	temperate	(147, 148, 149)
Hh 1	Halobacterium sp.	complex	linear	37.2	temperate	(110)
Hh3	Halobacterium sp.	complex	linear	29.4	temperate	(110)
la1	H.halobium	complex	linear	230	n.d.	(152)
S45	Halobacterium sp.	complex	linear	n.d.	n.d.	(21)
VLP(A3)	Methanococcus voltae A3	lemon	ccc	23	temperate	(161)
PG	Methanobrevibacter smithii G	complex	n.d.	50	lytic	(3)
PMS1	M.smithii	n.d.	n.d.	35	lytic	(76)
<b>∕M</b> 1	Methanobacterium thermoautotrophicum Marburg	complex	linear	27.1	lytic	(65, 92)
ÞF1	Methanobacterium sp.	complex	linear	85	lytic	(108)
ÞF3	M.thermoformicicum FF3	complex	ccc	36	lytic	(108)

a Covalently closed circular

dependent Sulfolobus shibatae (86) is one of the archaeal viruses studied in detail on the molecular level. Initially described as VLP, SSV1 was recently shown to infect the closely related S. solfataricus and is thus a true virus (130). The virus SSV1 contains a circular, positively supercoiled (97) double-stranded DNA genome with a size of 15.5 kb. Its complete nucleotide sequence has been determined (109) and the transcriptionally active regions have been mapped (123). Upon lysogenisation, the SSV1 genome is either maintained as extrachromosomal, autonomous replicating DNA (formerly termed pSB12) or is integrated into the chromosome (164). Integration occurs site-specifically in both S. shibatae and S. solfataricus within a putative tRNA<sup>Arg</sup> gene (124, 130). UV-irradiation induces amplification and packaging of the SSV1 plasmid form and the release of phage particles without lysis of the host (86, 130, 164). Since efficient transfection (106 transfectants per μg

<sup>&</sup>lt;sup>b</sup> The VLP-B6 genome is suggested to correspond with plasmid pBG (172).

c Not determined.

<sup>&</sup>lt;sup>d</sup> The DAV 1 genome is identical with plasmid pSL10 (172).

So-called 'carrier state' defined as an equilibrium between virus and cell multiplication. A shift of this equilibrium results in either loss of the phage genome or induction of the lytic circle (172).

f Several strains of H.halobium belong to the species H.salinarium (146).

g Consisting of an icosahedric head and a tail.

DNA) of S. solfataricus with SSV1 DNA by electroporation has been demonstrated (130), the well-studied SSV1 genome may be instrumental in developing a cloning vector for Sulfolobus.

Four rod-shaped or filamentous viruses, designated TTV1 through TTV4, have been described for *Thermoproteus tenax* Kra1 (63). Although these viruses exhibit a similar morphology they clearly differ in several aspects. TTV2 is a temperate virus, whereas TTV4 is lytic, while cells carrying TTV1 may either lyse or lose the virus (172). The viral genomes consist of linear, double-stranded DNA molecules of different size that showed no homology with each other (169). Moreover, only limited similarities have been observed in the composition of the virus envelope (169). TTV1 has been studied in most detail. The TTV1 DNA is covered by two DNA-binding proteins contained within the proteinaceous inner envelope that is surrounded by a asymmetric membrane (172). The genes encoding the two DNA-binding and the three major structural proteins of TTV1 have been analyzed (98, 172). Six genomic variants of TTV1 could be isolated that differed from each other in a distinct region by deletions and insertions (99). Since a phage-resistant strain of *T.tenax* contains part of this region integrated into its chromosome, it may specify immunity functions (172). Sequence analysis of the region revealed an unusual 465-bp ORF that could code for a protein with highly repeated amino acid stretches (169).

Three VPLs have been isolated from sulfur-dependent Archaea, CWP from the hyperthermophilic Pyrococcus woesei, DAV1 from Desulfurolobus ambivalens and a VPL from Sulfolobus strain B6. Since no nucleic acids could be isolated from CWP particles the nature of their genome remains unknown (170). Similarly, no data are available that clearly prove the association of the VPLs produced by Sulfolobus B6 with the genetic variable 35-kb plasmid pBG detected in the host (143, 172). In contrast, nucleic acids isolated from DAV1 particles seem to correspond with the 7.7-kb plasmid pLS10 of Desulfurolobus ambivalens, an extremely thermophilic, facultatively anaerobic archaeon (167, 168, 172). Interestingly, pLS10 shares some similarity with SSV1 DNA (172). Since anaerobic growth of the host is accompanied with amplification of plasmid pSL10 and the production of virus-like particles, pLS10 probably represents the lysogenic form of the virus DAV1 (169).

Phages isolated from the halophilic branch of the Archaea differ considerably in their genome sizes ranging from 30 kb for phage Hh3 (110) up to 230 kb reported for phage Ja1 (152). One of the most extensively studied halophilic virus-host systems is that of phage  $\Phi H$ and its host Halobacterium halobium R<sub>1</sub> (131, 172). The linear 59-kb genome of the temperate phage  $\Phi H$ , whose transcription units have been mapped (172), is circularized upon lysogenization and maintained as extrachromosomally replicating prophage (135). Similar to the genome of its host, a high degree of genetic variability has been observed for  $\Phi H$  that is due to the presence of certain IS-elements (132). One of these elements, ISH1.8 (134; see below), has been found to flank a central 12-kb fragment, called L-region, whose inversion or looping out is mediated by ISH1.8 (132, 134). The L-region contains genes for both immunity and the lytic cycle and obviously specifies all functions necessary for replication that enables the L-plasmid to be stably maintained in its host (see also plasmid section). Efficient transfection (approximately 10<sup>7</sup> transfectants per μg DNA) of H.halobium with ΦH DNA has also been reported based on a protocol similar to those used for plasmid transformation of halobacteria (15; see plasmid section). DNA modification has been described for another phage from H. halobium,  $\Phi N$ , whose linear, 56-kb genome contains 5methyl-cytosine (151).

A variety of viruses and VLPs have been described for methanogenic bacteria (for review:

172; Table 2). VLPs were found to accumulate during growth of Methanococcus voltae A3 (161). Similar to the prophage state of SSV1 in Sulfolobus shibatae, the genome of the M.voltae A3-derived VLPs which is a circular 23-kb DNA molecule, termed pURB600. could be detected either as free plasmid or integrated into the chromosome of its host. In addition, pURB600-related sequences have been identified in the chromosome of M. voltae PS which, however, did not produce VPLs (161). Plasmid pMP1 of Methanolobus vulcani (see plasmid section) may also represent a prophage since it has been found integrated into the host chromosome (155). The isolation of two lytic phage particles infecting Methanobrevibacter smithii, the broad host range phage PG (3) and phage PMS1 (76), with genome sizes of 50 and 35 kb, respectively, has been reported. The model virus-host system of methanogens that has been studied in some detail is that of the lytic phage  $\psi M1$  and its host Methanobacterium thermoautotrophicum Marburg (92). The genome of phage  $\psi M1$  is a linear, circularly permutated 27.1-kb DNA molecule that displays a terminal redundancy of approximately 3 kb (65). Packaging of the phage DNA is initiated from a concatemeric precursor molecule at a mapped pac site by the 'headful packaging' model (65). Interestingly, about 15% of the \$\sqrt{M}\$1 phage particles was found to contain hexamers of the cryptic 4.4-kb plasmid pME2001 present in the strain Marburg (88, 92). This relaxed packaging machinery of \$\psi M1\$ may be responsible for the recently demonstrated general transduction of chromosomal markers mediated by  $\psi$ M1 (93). A 16-kb chromosomal region with homology to \$\psi M1 DNA was identified in M. wolfei suggesting that this organism contains a deletion derivative of  $\psi M1$  (92). This may explain the similarity of the endopeptidases capable to hydrolyse pseudomurein-based cell walls that have been purified from lysates of autolysed M. wolfei cultures (71) and lysates produced by M. thermoautotrophicum Marburg after  $\psi M1$ infection (142).

# **Insertion sequences**

Most archaeal IS elements have been isolated from halophilic organisms, whereas only one IS elements have been reported for methanogens (Table 3). So far no information is available about such mobile elements in extreme thermophilic, sulfur-dependent *Archaea*.

The biology of IS elements has intensively been studied in the halophilic model organism *Halobacterium halobium*. *H.halobium* displays a considerable genetic instability that results in high spontaneous mutation rates of phenotypic markers such as gas vacuole formation and synthesis of the purple membrane protein bacterio-opsin which are lost with frequencies of  $10^{-2}$  and  $10^{-4}$ , respectively (113, 153). Most of these mutants were shown to result from genomic rearrangements such as insertions, deletions and recombination events induced by various IS-elements (22, 24, 25, 115, 116, 138). As indicated by further studies, the majority of these transposable elements and other repeated sequences are clustered within the relatively AT-rich satellite DNA fraction (GC-content 58%) consisting of plasmid DNA and chromosomal 'islands' that comprise about 30% of the genome of extreme halophilic organisms such as *H.halobium* (114, 118).

IS elements from halophiles (ISH elements; for review: 13) range in size from 520 bp for ISH2 up to 3000 bp for ISH24 (Table 3) and resemble in their structure 'typical' insertion sequences described for the bacterial domain (35), i.e., they contain terminal inverted repeats and are flanked by short direct repeats as the result of target site duplication (Table 3). ISH1.8 is an exception in that it lacks terminal inverted repeats (134). IS elements are defined as autonomously moving elements, i.e. they mediate their own transposition, which

Table 3. Archaeal insertion elements

Element	Host*	Element length (bp)	ORF <sup>6</sup> length (bp)	Copy number (bp)	IR <sup>e</sup> length (bp)	DR <sup>d</sup> length	Indentical copies*	References
ISH1	Halobacterium halobium <sup>(</sup>	1118	810	2	7	8	yes	(138)
ISH1.8	H.halobium	1895	max. 672 <sup>8</sup>	2	_	5	n.d.h	(134)
ISH2	H. halobium	520	_	8-10	19	10-11, 20	yes	(22)
ISH11	H.halobium	1068	1002	n.d.	15	7	n.d.	(81)
ISH23/50	H.halobium	996	819, 366	n.d.	19	9/8	n.d.	(115, 116, 163)
ISH24	H.halobium	3000	n.d.	2	14	7	n.d.	(115, 116)
ISH26	H.halobium	1384	441, 741	5	15	9, 11	no	(29)
ISH27	H.halobium	1398	1167	>2	16	5	no	(117, 120)
ISH28	H.halobium	932	0	>2	16	8	n.d.	(117, 121)
ISH S1	H.halobium	1449	1179, 366	n.d.	26	0	n.d.	(175)
ISH51	H. volcanii	1375	1146	20-30	16	3	no	(52, 120)
ISM1	Methanobrevibacter smithii	1381	1203	8-10	29	8	n.d.	(46)
FR-I	Methanobacterium thermoformicicum	1501	750 <sup>i</sup>	4-5	_	6	yes	(107)

<sup>&</sup>quot; Original host.

is catalyzed by an element-encoded transposase activity. Most of the ISH elements listed in Table 3 indeed contain at least one ORF that may encode a transposase-like protein. Some of the ISH elements, however, lack appropriate ORFs (Table 3) and probably represent non-autonomous IS elements that may transpose by transposase functions provided in *trans* by other, autonomous ISH elements. This may be the case for ISH51 from *Haloferax volcanii*. From three ISH51 elements that have been analyzed on the sequence level, only one was found to contain a large ORF (52, 120). Interestingly, ISH27 from *H.halobium* and ISH51 constitute a family of related insertion sequences that show identical terminal inverted repeats and considerable similarity on nucleotide sequence level of the entire elements (120). In the case of ISH2 which has an only low coding capacity (22), the existence of a copy with an intact function necessary for transposition seem to be unlikely since all so far analyzed ISH2 copies were identical on sequence level (119). However, the terminal inverted repeats of ISH2 are considerable similar to those found for ISH26 whereas the internal sequences of both elements lack homology (29). Since terminal inverted repeats play an important role in transposition of IS elements it was suggested that ISH26 mediates transposition of ISH2 (29).

Among methanogens only one transposable element, ISM1 from *Methanobrevibacter smithii*, has been characterized previously (46; Table 3). ISM1, whose movement within the host genome has been demonstrated, shows all features of a 'typical' insertion elements and contains a large ORF that probably specifies the transposase function (46).

<sup>&</sup>lt;sup>b</sup> Open reading frames with more than 300 bp.

<sup>&</sup>lt;sup>c</sup> Terminal located inverted repeats.

d Direct repeats flanking the element.

<sup>\*</sup> Nucleotide sequence idendity of different copies.

Several strains of H.halobium belong to the species H.salinarium (146).

<sup>&</sup>lt;sup>8</sup> ISH1.8 contains six ORFs with a size of more than 300 bp.

h not determined.

FR-I exists in two structural variants one of which contains a 750 bp ORF.

#### **OUTLINE OF THE THESIS**

The limited knowledge about plasmid biology of methanogens on the one hand and the need for developing host-vector system in this branch of Archaea on the other hand, were the principal motives to initiate the present thesis. Accordingly, the project had a basic character and was aimed at analyzing newly isolated plasmid DNA from methanogenic bacteria on molecular level with emphasis on those plasmids harbored by thermophilic strains of the genus Methanobacterium. After a brief summary of the state of art (Chapter 1), a phylogenetic analysis of different thermophilic Methanobacterium strains including several new isolates is described in Chapter 2. The obtained results from sequence comparison of PCR-amplified 16S rRNA genes strongly suggested a reclassification of the species M. thermoformicicum and M. thermoautotrophicum. The following Chapters 3 and 4 deal with the characterization of two types of mobile elements, namely phages and plasmids. The isolation and characterization of two novel phages,  $\Phi$ F1 and  $\Phi$ F3, capable of infecting several thermophilic Methanobacterium strains is reported in Chapter 3. Phage  $\Phi$ F1 whose linear genome is approximately 80 kb in size, has a broad host range and could be propagated on M.thermoformicicum Z-245, FTF, FF1, FF3 and CSM3 as well as M.thermoautotrophicum  $\Delta H$ . In contrast, phage  $\Phi F3$  is specific for *M.thermoformicicum* FF3. Chapter 4 describes the isolation and characterization of a family of related plasmids from the thermophilic archaeon M. thermoformicicum and initial approaches in classification of M. thermoformicicum strains by genetic fingerprinting. Two of the plasmids, pFV1 from strain THF and pFZ1 from strain Z-245, were analysed in detail. Comparison of the complete nucleotide sequences of pFV1 and pFZ1 allowed an outline of the genetic organization of the plasmid genomes consisting of conserved regions which are interspersed with accessory elements (Chapter 5). Moreover, evidence is provided that plasmid pFV1 encodes a putative DNA mismatch repair which is functionally related to the pFV1-borne restriction-modification (R/M) system (Chapter 5). One of the accessory elements, termed FR-I, was present in the genomes of strains of M.thermoformicicum and M.thermoautotrophicum (Chapter 6). Although transposition of FR-I has not been demonstrated, several characteristics of FR-I support the hypothesis that it represents a new type of archaeal insertion elements. In addition, pFV1 and pFZ1 were found to contain an accessory element encoding components of different R/M systems, whose detailed analysis is discussed in Chapter 7 and 8, respectively. Finally, a summary and concluding remarks are given in Chapter 9.

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# Phylogenetic analysis of thermophilic *Methanobacterium* sp.: evidence for a common formate-utilizing ancestor

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#### SUMMARY

Comparative sequence analysis of PCR-amplified 16S rRNA genes from members of *M.thermoformicicum* and *M.thermoautotrophicum* provide evidence that the classification into these two species does not reflect their phylogenetic relationship. Our results support the proposal of Touzel and coworkers (1992) who, based on DNA hybridization and immunological studies, identified at least three groups among strains of *M.thermoformicicum* and *M.thermoautotrophicum* which may represent different species. Those three groups comprise (i) *M.thermoformicicum* strains Z-245, FTF, THF, CSM3, FF1 and FF3, and *M.thermoautotrophicum*  $\Delta$ H, (ii) *M.thermoformicicum* strains CB12, SF-4 and HN4, and (iii) *M.thermoautotrophicum* Marburg. In addition, sequences related to the *fdhA* and *fdhB* genes for formate dehydrogenase were identified in the genomes of *M.thermoautotrophicum* strains  $\Delta$ H and Marburg suggesting that *M.thermoautotrophicum* and *M.thermoformicicum* have been derived from a common ancestor able to utilize formate.

#### INTRODUCTION

The thermophilic species Methanobacterium thermoautotrophicum and Methanobacterium thermoformicicum are classified according to their ability to use H<sub>2</sub>/CO<sub>2</sub> only or H<sub>2</sub>/CO<sub>2</sub> and formate, respectively, as sole energy- and carbon source (Whitman et al., 1992). Several observations suggest, however, that a taxonomy based on a phenotypical character such as formate-utilization may not reflect the phylogenetic relationship of the two species. The assignment of M.thermoautotrophicum strains ΔH and Marburg into the same species was questioned already more than ten years ago by Brandis et al. (1981) who found that the strains ΔH and Marburg exhibit only limited (46%) DNA-DNA relatedness and show considerable differences in composition of cell wall amino sugars and the large subunit of the DNA dependent RNA polymerase. M.thermoformicicum strains, on the other hand, differ in respect to immunological cross-reactions (Yamamoto et al., 1989) and genetic fingerprinting (Nölling et al., 1991). Moreover, comparison of 5S rRNA sequences (Chumakov et al., 1987) and immunological studies (Bezrukova et al., 1989) indicate that M.thermoautotrophicum ΔH is closer related to M.thermoformicicum Z-245 than to M.thermoautotrophicum Marburg.

The question whether the strains of M.thermoautotrophicum and M.thermoformicicum have to be reclassified should be answered by a detailed analysis of their similarity on nucleic acid level, e.g. by DNA-DNA hybridization studies and ribosomal RNA sequence comparisons. The recently reported results from DNA-DNA similarity values and immunological studies of several strains of the species M.thermoautotrophicum and M.thermoformicicum (Touzel et al., 1992) clearly indicate that reclassification of both species is required. It was found that (i) M.thermoautotrophicum  $\Delta H$  is only distantly related to M.thermoautotrophicum Marburg but more related to some members of the species M.thermoformicicum, and (ii) the species M.thermoformicicum includes strains which may belong to another, not yet defined species (Touzel et al., 1992).

One of the powerful methods to determine the evolutionary relationship among different organisms is the analysis of the variable regions of small subunit rRNAs sequences (Woese et al., 1987). Among the thermophilic strains of the genus Methanobacterium, only the rRNA operon of M.thermoautotrophicum Marburg has so far been characterized in detail by sequence analysis of a genomic clone (Østergaard et al., 1987). The aim of the present report was to analyze the differences in the 16S rRNA of members of Methanobacterium in order to confirm their inter- and intraspecies relationship derived from DNA-DNA similarity studies (Touzel et al., 1992). For this purpose, we determined the partial 16S rRNA sequences of M.thermoautotrophicum  $\Delta H$  and M.thermoformicicum strains Z-245, FTF, THF, CB12, SF-4, FF1, FF3, CSM3 and HN4 from cloned 16S rRNA genes that were amplified by the polymerase chain reaction (PCR), and compared these sequences with that of the 16S rRNA from M.thermoautotrophicum Marburg. Furthermore, we show that the non-formate utilizing strains M.thermoautotrophicum Marburg and  $\Delta H$  contain sequences related to the genes encoding the  $\alpha$  and  $\beta$  subunit of the formate-dehydrogenase (fdhA and fdhB, respectively) from M.formicicum.

#### MATERIAL AND METHODS

### Methanogenic strains

The following strains were obtained from the German Collection of Microorganisms (Braunschweig, Germany): M.thermoautotrophicum  $\Delta H$  (DSM 1053), M.thermoformicicum strains Z-245 (DSM 3720), FTF (DSM 3012), THF (DSM 3848) and CB12 (DSM 3664). M.thermoformicicum SF-4, kindly provided by K. Yamamoto, Japan, and strains FF1 and FF3 have been described previously (Nölling et al., 1991). M.thermoformicicum strains CSM3 and HN4 were isolated according to previously described procedures (Nölling et al., 1991) from a mesophilic upflow-anaerobic-sludge-bed reactor (T. Grotenhuis and C. Plugge, Department of Microbiology, University of Wageningen, The Netherlands) and from sediment of the river Rhine collected nearby Wageningen, The Netherlands, respectively.

### PCR amplification of 16S rRNA-genes

Total DNA from methanogenic bacteria was isolated as described previously (Nölling et al., 1991).

To facilitate cloning of PCR products, two primers commonly used for reverse transcriptase sequencing (Embley et al., 1988) were synthesized with a 5' extension containing an unique

restriction enzyme cleavage sites. Primer 1510 (Embley et al., 1988) was equipped with a PstI-site resulting in primer 1510Pst with the sequence 5'-GTGCTGCAGGGTTACCTTGTTACGACT (complementary to position 1493 to 1510 in the Escherichia coli numbering system). The second primer, 124Bam, complementary to primer 124 (Embley et al., 1988), contained an additional BamHI-site and had the sequence 5'-CACGGATCCGGACGGGTGAGTAACACG (position 106 to 124 in the E.coli numbering system).

PCR was performed in a total volume of 100  $\mu$ l containing 10  $\mu$ l 10 x PCR buffer (500 mM KCl, 25 mM MgCl<sub>2</sub>, 200 mM Tris/HCl pH 8.4, 1 mg/ml gelatine, 0.001% Nonidet P-40), 1  $\mu$ l dNTPs (each 10 mM in 10mM Tris/HCl pH 7.5), 0.2  $\mu$ l Taq polymerase (5 U/ $\mu$ l, Life Technologies Inc, Gaithersburg, Md.), 1  $\mu$ l of each of the primers 1510Pst and 124Bam (100 ng/ $\mu$ l), and 1  $\mu$ l DNA preparation (approximately 100 ng). Thirty rounds of temperature cycling (95°C for 1 min, 48°C for 2 minutes and 72°C for 3 minutes) were followed by a final 7 min step at 72°C.

# Cloning and sequencing of amplified PCR products

The amplification products were treated with proteinase K (0.1 mg/ml, Boehringer Mannheim, FRG) according to Crowe et al. (1991) except that sodium dodecyl sulfate (SDS) was added to a final concentration of 0.5% followed by an incubation at 55°C for 20 min. Subsequently, the suspension was extracted with phenol/chloroform, and the DNA was precipitated with ethanol and finally dissolved in TE buffer (10 mM Tris/HCl pH 8.0, 1 mM EDTA). The amplified DNA was digested with BamHI and PstI (Life Technologies Inc., Gaithersburg, Md.), separated by agarose gel electrophoresis and purified by the Geneclean procedure (Bio 101, La Jolla, Calif.). Cloning of the amplification products into BamHI/PstI-digested phage M13mp18/19 (Yanisch-Perron et al., 1985) and isolation of double- and single-stranded M13-DNA was done by standard methods (Sambrook et al., 1989), using E.coli TG1 (Gibson, 1983) as host.

The nucleotide sequences of overlapping fragments derived from the cloned amplification products were determined by the dideoxy chain termination method (Sanger et al., 1977) using the Sequenase kit according to the manufacturer's instructions (United States Biochemical Corp. Cleveland, Ohio). In addition to the supplied M13-forward sequencing primer, two new primers were synthesized for determination of the internal sequence of the cloned amplification products: primer 361 with the sequence 5'-GGGGCGCAGCAGCGCC corresponding to positions 346 to 361 (E.coli numbering system) and primer 1114 with the sequence 5'-GGGTCTCGCTCGTTGCC complementary to positions 1098 to 1114 (E.coli numbering system). The 16S rRNA sequence of each strain used for comparison was based on two different clones derived from the same PCR reaction, or - in the case of M.thermoformicicum strains Z-245, THF, CSM3, FF1 and HN4, and M.thermoautotrophicum ΔH - from independent PCR reactions.

#### DNA hybridization

For the detection of formate-dehydrogenase-related sequences present in the genomes of different *Methanobacterium* strains a radioactively labelled 2.2-kb *BamHI-SphI* fragment containing the *fdhA* gene or a 1.8-kb *BamHI-SphI* fragment containing the *fdhB* gene from *M.formicicum JF-1* (Shuber et al., 1986; kindly provided by J. G. Ferry, Department of

Anaerobic Microbiology, VPI Blacksburg, VA 24061, USA) were used as probes. Total DNA prepared from *Methanobacterium* strains was digested, electrophoresed on a 0.7% agarose gel, and transferred to a Hybond-N nylon filter (Amersham, United Kingdom) by the capillary blot procedure (Sambrook et al., 1989). Prehybridization of the nylon membranes was performed at 65°C for 15 min in 0.5 M NaHPO<sub>4</sub> pH 7.2, 1 mM EDTA, 7% SDS, 1% serum albumin and 0.5 mg sonicated and denaturated salmon sperm DNA. After purification from agarose gel, the DNA probe was radioactively labelled by nick-translation (Sambrook et al., 1989) with  $[\alpha^{-32}P]$ dATP (110 TBq/mmol; Amersham, United Kingdom), denaturated and added to the prehybridization solution. Hybridization was performed at 55°C for 18 h. The membranes were washed for 5 min at room temperature in 2 x SSC (0.3 M NaCl, 0.03 M sodium citrate) containing 0.1% SDS, followed by incubation in the same buffer for 20 min at 55°C and were finally subjected to autoradiography.

#### RESULTS AND DISCUSSION

## Hybridization with fdh genes

Among the thermophilic species of the order *Methanobacteriales*, only *M.thermoformicicum* is able to convert formate, whereas *M.thermoautotrophicum* strains have not been reported to utilize formate (Whitman et al., 1992). We have previously shown that comparison of hybridization patterns derived from probing with fdhA, the structural gene coding for the  $\alpha$  subunit of formate hydrogenase of the mesophilic *M.formicicum* (Shuber et al., 1986), is a useful technique for the classification of *M.thermoformicicum*. Two groups could be distinguished using this approach: the Z-245-group comprising strains Z-245, FTF, THF, FF1, and FF3, and the CB12-group including strains CB12 and SF-4 (Nölling et al., 1991). The two new *M.thermoformicicum* isolates CSM3 and HN4 were classified in the same way (data not shown) and found to belong to the Z-245-group and the CB12-group, respectively.

Unexpectedly, we found that radioactively labelled fdhA hybridized also with total DNA of the non-formate utilizers M. thermoautotrophicum strains  $\Delta H$  and Marburg (Fig. 1A). Moreover, M. thermoautotrophicum strains  $\Delta H$  and Marburg also contained genomic sequences homologous to fdhB (Fig. 1B), which encodes the  $\beta$  subunit of the M. formicicum formate dehydrogenase (Shuber et al., 1986). The hybridization signals obtained with radioactively labelled fdhA and fdhB revealed a hierarchy of intensity in which the most intense signals were found with DNA from M. thermoautotrophicum  $\Delta H$  DNA were stronger than those with DNA from M. thermoautotrophicum Marburg (Fig. 1).

The hybridization data clearly show that the genomes of M. thermoautotrophicum strains  $\Delta H$  and Marburg contain fdh-related sequences suggesting that the inability of both strains to convert formate is due to a non-functionality of the fdh-operon rather than the absence of the structural genes for formate dehydrogenase. If so, the non-functionality of the fdh genes in the M. thermoautotrophicum strains may explain the observed less intense hybridization signals compared to those obtained with DNA from members of the only distantly related formate-utilizing M. thermoformicicum Z-245- and CB12-group (Fig. 1): the selective pressure on the latter strains should ensure conservation of the fdh genes whereas mutations in the non-essential fdh-related sequences of M. thermoautotrophicum strains  $\Delta H$  and Marburg would not have been selected out.

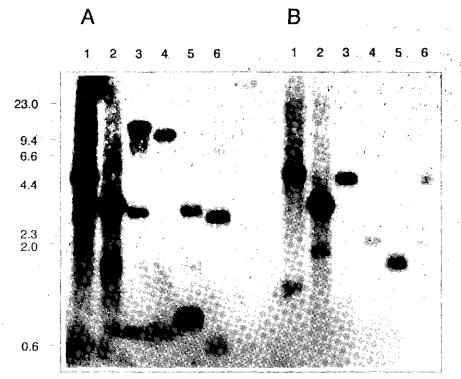


Figure 1. Southern hybridization of total DNA isolated from Methanobacterium with the M.formicicum fdhA (panel A) and fdhB genes (panel B). Total DNA (about 0.5  $\mu$ g each) was isolated from M.thermoformicicum FTF (lane 1) and SF-4 (lane 2), and M.thermoautotrophicum strains  $\Delta$ H (lane 3, 5) and Marburg (lane 4, 6), digested with BamHI (lanes 1-4) and BamHI/SphI (lanes 5, 6) and separated by agarose gel electrophoresis. After transfer of the DNA to nylon-membranes, the blots were hybridized with a radioactively labelled 2.2-kb BamHI-SphI fragment containing the fdhA (panel A) and a 1.8-kb BamHI-SphI fragment containing the fdhB gene (panel B) from M.formicicum JF-1. The sizes (in kilobases) of HindIII  $\lambda$  DNA fragments are indicated at the left.

The presence of cryptic fdh genes implies that the strains  $\Delta H$  and Marburg were derived from ancestors that were able to convert formate. M.thermoautotrophicum  $\Delta H$  is closely related on genomic level to the M.thermoformicicum Z-245-group (Touzel et al., 1992; see below) and therefore represents a non-formate utilizing member of M.thermoformicicum. Strain Marburg, in contrast, is only distantly related to the thermophilic formate-utilizing Methanobacterium strains (Touzel et al., 1992; see below). Since both M.thermo-autotrophicum strains harbor cryptic fdh genes, it is reasonable to assume that M.thermoformicicum and M.thermoautotrophicum strains  $\Delta H$  and Marburg have been originated from a common formate-utilizing ancestor. Interestingly, a similar diversity in the ability to convert formate in addition to  $H_2/CO_2$  is typical among mesophilic Methanobacterium strains and members of the closely related genus Methanobrevibacter (Whitman et al., 1992). It is therefore tempting to speculate that the non-formate utilizers among those strains also contain cryptic fdh genes. If so, this would imply that the capacity to convert formate into methane has occurred early in evolution of the genus Methanobacterium and its close relatives.

# 16S rRNA sequence analysis

Using PCR-amplified templates, partial 16S rRNA nucleotide sequences were determined from M.thermoautotrophicum  $\Delta H$  and nine M.thermoformicicum strains including all seven strains reported so far and the two new isolates described here. The sequencing strategy generated a continuous stretch of 1334 bases of each strain. The 16S rRNA sequences from the nine strains examined were aligned with that of M.thermoautotrophicum Marburg (Ostergaard et al., 1987; Fig. 2). For calculation of the similarity values the 16S rRNA sequence of the mesophilic formate-utilizer M.formicicum was included (Table 1). Based on the derived  $K_{nuc}$  (evolutionary distance) values an unrooted phylogenetic tree was constructed

			VR1		
115					
	UAACCCCGGGAAAC	UGGGGAUAAACCUG	GATAGGUGAUGCGG	CCUGGAAUGGUGCU	NUCACCGAAACACCUUCGGGGUGCCCAA
					C
					C
231	261	551	711	971	1061
GGUAGUUGGU	CCAUCAUCGG	AUCCCGCAGC	AAGCUAGGGG	UUGCCUGACG	CCUUAGUUACCAGCGGGACCCUUUGGGGUU
U	.G	<i>.</i>	C		AU
U	.G	A	C.,,,		
	.G	A	C		AUAAU
U	.G	A	C		AUAAU
	.G	A	C		
U	. G	<del>,</del>	C	********	
	.G		C		AU
•••••	•••••	<u>A</u>	Ç	UA	AU
********	********		<u>c</u>	UA	AU
•••••	*********	A	C	UA	AAAU
			VRI	<u> </u>	Accession numbers or source of
					16S rRNA sequence
1211	1271	1311	1386		
CGACACUGAA	ACUCGECEUC	CAUUAUCGCG	GGCCACAGUAUU		Østergaard et al. (1987)
	<u>c</u>	<u>c</u>	AC		x68720
	<u>c</u>	c	AC		x68712
c	<u>c</u>	<u>c</u>	AC		x68713
<u>C</u>	<u>c</u>	<u>C</u>	AC		x68714
	<u>c</u>	<u>c</u>	AC		X68715
<u>Ç</u>	<u>c</u>	C	AC		X68716
	C				x68711
		********			X68717
• • • • • • • • • • • • • • • • • • • •	********	• • • • • • • • • • • • • • • • • • • •			X68718
		********		U	x68719

Figure 2. Alignment of variable regions of 16S rRNA sequences derived from M.thermoautotrophicum Marburg (Østergaard et al., 1987) and  $\Delta H$ , and M.thermoformicicum strains Z-245, FTF, FF1, FF3, CSM3, THF, CB12, SF-4 and HN4. Base positions in the sequences are numbered consecutively and correspond to the numbering of the 16S rRNA from strain Marburg (Østergaard et al., 1987). Only nucleotides that differ from strain Marburg are shown, while identical nucleotides are denoted by dots. (-) correspond to alignment gaps. Regions VRI and VRII represent highly variable regions. The accession numbers (EMBL database) assigned to the analyzed 16S rRNA sequences are indicated.

using the neighbor-joining method of Saitou and Nei (1987) (Fig. 3).

The determined 16S rRNA sequences of the examined thermophilic Methanobacterium strains were highly similar ranging from 98.5 to 100%. In total 29 positions were found to be variable and a maximum of 19 base variations were observed between two sequences (Fig. 2). The majority (16) of those base variations was concentrated in two highly variable regions, designated VRI (position 122 to 200 according to the numbering of the 16S rRNA from M. thermoautotrophicum Marburg [Østergaard et al., 1987]) and VRII (position 1393) to 1401), which are located close to the 5'- and 3'-terminus of the 16S rRNA molecule. respectively (Figures 2 and 4). Alignment of the variable positions of the 16S rRNA molecules allowed the recognition of different 16S rRNA signatures and a classification of the corresponding Methanobacterium strains into at least three groups with nearly identical 16S rRNA sequences. One of these groups is represented by M.thermoautotrophicum Marburg. The two other groups are coinciding with those derived from genetic fingerprinting with fdhA (see above), i.e. the Z-245-group, comprising M. thermoformicicum strains Z-245, FTF, FF1, FF3 and CSM3, and the CB12-group, consisting of M, thermoformicicum strains CB12. SF-4 and HN4. Based on the 16S rRNA similarity. M. thermoautotrophicum  $\Delta H$ belongs to the Z-245-group.

The 16S rRNA sequences of the Z-245- and the CB12-group differ from each other at 17 positions, corresponding to 98.7% sequence similarity. Both differ from *M.thermo-autotrophicum* Marburg at 19 positions, corresponding to 98.6% sequence similarity. *M.thermoformicicum* THF has a slightly different 16S rRNA signature which shows similarity with those of all three groups. Its close proximity to the Z-245 branch suggests, however, that strain THF should be assigned to the Z-245 group as proposed on the basis of DNA-DNA hybridization studies (Touzel et al., 1992).

Using the secondary structural model of the 16S rRNA molecule of *M.thermoautotrophicum* Marburg (Østergard et al., 1987), the variable positions of the examined 16S rRNA sequences were analyzed for their possible effect on secondary structure. As illustrated in Figure 4 for the two highly variable regions VRI and VRII, about one third of the base

ble 1. Percentages of similarity (upper right) and K<sub>me</sub> values (lower left) for a 1334 bp region of 16S rRNAs from strains of the genus Methanobacterium

Organism	1.	2.	3.	4.	<b>5</b> .	6.	7.	8.	9.	10.	11.	12.
. M.thermoautotrophicum Marburg	_	98.6	98.7	98:6	98.7	98.6	98.7	98.9	98.6	98.6	98.5	92.3
. M. thermoautotrophicum ΔH	0.0141	_	99.9	100.0	99.9	100.0	99.9	99.5	98.8	98.8	98.7	92.0
. M.thermoformicicum Z-245	0.0133	0.0001		99:9	100.0	99.9	100.0	99.5	98.7	98.7	98.6	92.0
. M.thermoformicicum FTF	0.0141	0.0	0.0001	_	99.9	100.0	99.9	99.5	98.8	98.8	98.7	92.1
. M.thermoformicicum FF1	0.0133	0.0001	0.0	0.0001	_	99.9	100.0	99.5	98.7	98.7	98.6	92.0
. M.thermoformicicum FF3	0.0141	0.0	0.0001	0.0	0.0001		99.9	99.5	98.8	98.8	98.7	92.1
. M.thermoformicicum CSM3	0.0133	0.0001	0.0	0.0001	0.0	0.0001	_	99.5	98.7	98.7	98.6	92.0
M.thermoformicicum THF	0.0110	0.0045	0.0053	0.0045	0.0053	0.0045	0.0053	_	98.9	98.9	98.9	92.3
M.thermoformicicum CB12	0.0141	0.0122	0.0129	0.0122	0.0129	0.0122	0.0129	0.0107	_	100.0	99.9	92.4
. M.thermoformicicum SF-4	0.0141	0.0122	0.0129	0.0122	0.0129	0.0122	0.0129	0.0107	0.0	_	99.9	92.4
. M.thermoformicicum HN4	0.0148	0.0129	0.0137	0.0129	0.0137	0.0129	0.0137	0.0114	0.0001	0.0001	_	92.3
. M. formicicum (DSM 1312)	0.0816	0.0841	0.0849	0.0832	0.0849	0.0831	0.0848	0.0808	0.0801	0.0801	0.0808	-

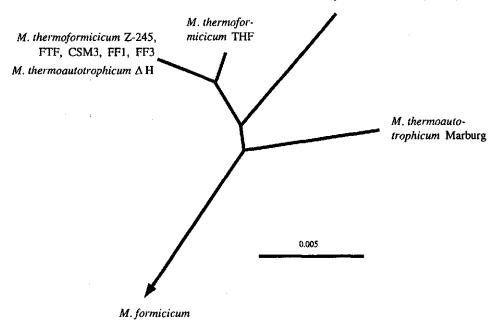


Figure 3. Phylogenetic tree reflecting the intrageneric relationships of Methanobacterium strains.

variations affected unpaired sequence regions that do not contribute to the stability of the secondary structure. In contrast, the other two third of the base substitutions were located in helical regions and most of those may affect the secondary structure of the 16S rRNA since only one position of a base pair was changed. Interestingly, the majority of those non-compensatory base substitutions affected mispaired regions in the 16S rRNA of *M.thermoautotrophicum* Marburg and generated perfect base pairing in the 16S rRNA sequences of members of the Z-245 and the CB12 group. Inspection of all variable positions located in helical regions of the analyzed 16S rRNAs of *M.thermoformicicum* and *M.thermoautotrophicum*  $\Delta H$  revealed that this is true for the majority of base substitutions (Table 2).

Two conclusions may be drawn from the 16S rRNA sequence comparison. Firstly, the species M.thermoformicicum consists of two groups of strains, the Z-245- and the CB12-group, whose degree of phylogenetic relationship is as high as the relationship between each of these groups and M.thermoautotrophicum Marburg. Secondly, M.thermoautotrophicum  $\Delta H$  is phylogenetically closer related to members of the Z-245-group than to M.thermoautotrophicum Marburg.

The obtained 16S rRNA data are in congruence with the results derived from DNA-DNA hybridization studies and antigenic fingerprinting described by Touzel et al. (1992) and support their conclusions that the examined strains of *M.thermoautotrophicum* and *M.thermoformicicum* comprise at least three groups of considerable similar strains. As shown in Table 3, the *M.thermoformicicum* strains Z-245 and CB12 on the one and *M.thermo-autotrophicum* Marburg on the other hand exhibit about 30% DNA-DNA similarity. Based

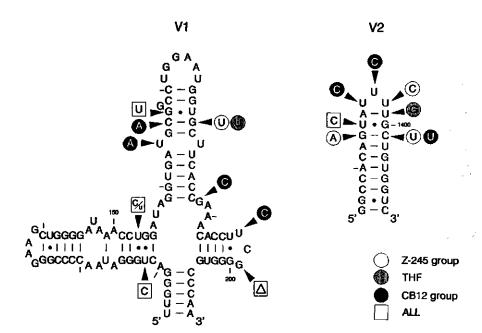


Figure 4. Secondary structure of the two variable regions VRI and VRII (see Fig. 2) of 16S rRNA sequences from strains of *M.thermoautotrophicum* and *M.thermoformicicum*. The secondary structure shown is that from *M.thermoautotrophicum* Marburg (Østergaard et al., 1987). Variable positions found in the 16S rRNA sequences from members of the Z-245- and CB12-group and from strain THF are indicated. A deleted nucleotide is denoted by ( $\Delta$ ). At position 153, the substitution (C) for (U) found for the majority of the strains is indicated.

Table 2. Variable base pairs in 16S rRNA from strains of the genus Methanobacterium

Position of	M.thermoautotrophicum	M.thermo	M.formicicum	
base pair	Marburg	CB12-group	Z-245-group <sup>b</sup>	
122:154	Ŭ∙G	C:G	C:G	U∙G
123:153	G·U	G:C	G:Y°	G:C
164:182	Ùυ	A:U	บบ	G:C
166:180	C:G	A G	СU	C U
167:179	<b>G</b> ∙U	បប	บบ	บับ
556:568	G•U	A:U	A:U	A:U
715:752	U∙ <b>G</b>	C:G	C:G	C:G
955:975	G:C	G∙U	G:C	A:U
1077:1099	G∙U	A:U	A:U	G:C
1217:1222	U∙G	Ŭ∙G	C:G	U∙G
1393:1401	G:C	G:C	A:U	G∙U
1394:1400	U-G	C:G	C:G	U·G
1395:1399	A:U	A:U	A:Gd	C:G

<sup>\*</sup> Numbering follows M. thermoautotrophicum Marburg 16S rRNA.

b Including M.thermoautotrophicum ΔH.

<sup>°</sup> Y = pyrimidine.

<sup>&</sup>lt;sup>4</sup> M.thermoformicicum THF only.

on these low values it was proposed that those strains belong to different species (Touzel et al. 1992). In contrast, the strains whose 16S rRNA sequences were found to be most similar to that of *M.thermoformicicum* Z-245, i.e. those of the Z-245-group, exhibit DNA-DNA similarity values of more than 70% (Table 3). According to Wayne et al. (1987), this is sufficiently high to assign these strains to the same species as proposed by Touzel and coworkers (1992). Although no DNA-DNA hybridization data are available that compare members of the CB12-group with each other, their nearly identical 16S rRNA signatures suggest that those strains belong to the same species.

Table 3. Comparison between DNA-DNA hybridization results (Touzel et al., 1992) and the levels of 16S rRNA sequence similarity

Organism pair	% of DNA-DNA hybridization	% of 16S rRNA homology
M.thermoformicicum Z-245 and M.thermoformicicum CB12	25	98.7
M. thermoformicicum CB12 and M. thermoautotrophicum Marburg	27	98.6
M.thermoformicicum CB12 and M.thermoformicicum THF	27	98.9
M.thermoformicicum Z-245 and M.thermoautotrophicum Marburg	29	98.6
M.thermoformicicum THF and M.thermoautotrophicum Marburg	33	98.9
M.thermoformicicum Z-245 and M.thermoformicicum THF	73	99.5
M.thermoformicicum Z-245 and M.thermoautotrophicum ΔH	97	99.9

The present 16S rRNA sequence analysis confirms the recently proposed classification of several thermophilic *Methanobacterium* strains based on DNA-DNA similarity studies (Touzel et al., 1992) and allows to determine the phylogenetic relationship of the examined methanogens. Additional support for the new classification is provided by the fact that the obtained genomic relatedness of the three thermophilic *Methanobacterium* groups correlates well with the established antigenic relationships (Touzel et al., 1992). Moreover, the homogeneity of the Z-245-group including *M.thermoautotrophicum*  $\Delta H$  is supported by recent phage-typing studies using the newly identified *Methanobacterium* phage  $\Phi F1$  (Nölling et al., 1993a) and the presence of a specific DNA sequence possibly representing a mobile DNA element that was found to be restricted to strains of this group (Nölling et al., 1993b).

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 $\Phi$ F1 and  $\Phi$ F3, two novel virulent, archaeal phages infecting different thermophilic strains of the genus *Methanobacterium* 

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#### **SUMMARY**

Two virulent, archaeal phages,  $\Phi$ F1 and  $\Phi$ F3, were isolated that were capable of infecting different thermophilic members of Methanobacterium. Both phages exhibited a similar morphology consisting of a polyhedral head and a tail but differed considerably in their host specificities and the size and topology of their genomes. Phage  $\Phi F1$  contained a linear, double-stranded DNA genome of  $85 \pm 5$  kb in size and showed a broad host range including M. thermoformicicum strains Z-245, FTF, FF1, FF3 and CSM3, and M. thermoautotrophicum ΔH. In contrast, ΦF3 phage particles contained a circular genome, comprising approximately 36 ± 2 kb double-stranded DNA, and could only be propagated on M. thermoformicicum FF3. Hybridization experiments did not reveal similarity between the genomes of  $\Phi$ F1 and ΦF3 nor between both phages and genomic DNA from different thermophilic members Methanobacterium or from phage \$\psi M1\$ of M.thermoautotrophicum Marburg. A physical map of both phage genomes was constructed. The DNA of phage  $\Phi F1$  was found to contain multiple GGCC-sites which form the target for restriction-modification (R/M) system MthTI of M. thermoformicicum THF. Therefore, restriction of  $\Phi$ F1 DNA may explain the resistance of strain THF against infection by  $\Phi$ F1. In contrast, the ability of  $\Phi$ F1 to infect strains Z-245 and FTF both of which harbor CTAG-specific R/M systems, is probably due to the presence of only a single CTAG-site in the genome of  $\Phi$ F1.

# INTRODUCTION

A variety of viruses and virus-like particles have been found in representatives of the three major lines of the archaebacteria (now termed Archaea; Woese et al., 1990), the methanogenic, the halophilic and the extreme thermophilic, sulfur-dependent organisms (for review: Zillig et al., 1988). All archaeal viruses and virus-like particles characterized so far contain double-stranded DNA genomes with a size ranging from less than 30 kb found for those infecting extreme thermophilic, sulfur-dependent Archaea up to 230 kb for the phage Jal of Halobacterium halobium (Zillig et al., 1988; Wais et al., 1975).

One of the best studied archaeal phages is the lemon-shaped, temperate virus SSV1 from Sulfolobus shibatae whose circular, positively supercoiled 15.5-kb genome (Nadal et al., 1986) is maintained either free or integrated into the chromosome of its host (Yeats et al., 1982). The integration site (Reiter et al., 1989) and transcription units (Reiter et al., 1987) of the SSV1 genome have been mapped and its complete nucleotide sequence has been determined (Palm et al., 1991). Initially described as a virus-like particle which could not

be propagated on S.shibatae, SSV1 was recently shown to infect S.solfataricus and is thus a true virus (Schleper et al., 1992). Moreover, also transfection with SSV1 DNA has been demonstrated (Schleper et al., 1992). A temperate phage of the halophilic branch,  $\Phi$ H, has also successfully been used to transfect spheroplasts of its host Halobacterium halobium (Cline and Doolittle, 1987). The linear 59-kb  $\Phi$ H genome, whose transcription units were mapped (Zillig et al., 1986), is circularized upon lysogenization (Schnabel and Zillig, 1984b) and exhibits, similar to the genome of its host, a high degree of genetic variability (Schnabel et al., 1982) which is mediated by certain insertion elements, predominantly ISH1.8 (Zillig et al., 1988; Schnabel et al., 1984a). Similar to certain phages of the bacterial domain, modification of archaeal phage DNA has been observed for phage  $\Phi$ N of H.halobium whose linear, 56-kb genome was found to contain 5-methyl-cytosine (Vogelsang-Wenke and Oesterhelt, 1988).

For methanogens, at least one virus-like particle, isolated from *Methanococcus voltae* A3 (Wood et al., 1989) and a putative prophage of *Methanolobus vulcani* (Wilharm et al., 1986) have been described. Two infective phage particles were isolated from *Methanobrevibacter smithii*, the lytic phages PG (Bertani and Baresi, 1986) and PMS1 (M. R. Knox and J. E. Harris, Abstr. XIV Internat. Congr. Microbiol. 1986, P.G3-8, p. 240) with genome sizes of 50 and 35 kb, respectively. The best characterized phage of the methanogenic branch is  $\psi$ M1 from the thermophilic *Methanobacterium thermoautotrophicum* Marburg (Meile et al., 1989). This lytic phage contains a linear, circularly permutated 27.1-kb genome with a terminal redundancy of approximately 3 kb (Jordan et al., 1989). Interestingly, besides the concatemeric precursor of the phage DNA which is packaged by a headful mechanism, also multimers of the cryptic 4.4-kb plasmid pME2001 harbored by strain Marburg (Meile et al., 1983) could be isolated from  $\psi$ M1 particles (Meile et al., 1989). This relaxed packaging machinery is probably responsible for the recently demonstrated general transduction mediated by  $\psi$ M1 (Meile et al., 1990).

In the present study we report the isolation and initial characterization of two novel lytic archaeal phages,  $\Phi$ F1 and  $\Phi$ F3, capable of infecting different thermophilic strains of the genus *Methanobacterium*.

# MATERIAL AND METHODS

# Bacterial strains and phages

Strains of *M.thermoformicicum* and *M.thermoautotrophicum* used in this study are listed in Table 1. Cultivation of methanogenic strains in liquid cultures or on solidified 0.8% Gelrite plates (Roth GmbH, Karlsruhe, FRG) was performed as described previously (Nölling et al., 1991) except that  $0.2 \text{ g/l MgCl}_2$  was used. DNA of phage  $\psi$ M1 was a gift from L. Meile (Department of Microbiology, ETH Zürich, Switzerland)

# Isolation of methanogenic phages

For the isolation of both phages  $\Phi F1$  and  $\Phi F3$  samples were taken anaerobically from an upflow anaerobic sludge-bed reactor operating at 55°C (Department of Environmental Engineering, University of Wageningen, The Netherlands) which already had served as source for the isolation of *M.thermoformicicum* strains FF1 and FF3 (Nölling et al., 1991).

For enrichment of phages, 10 ml of the samples were sterilized by filtration on a 0.2  $\mu$ m filter (Schleicher & Schuell, Dassel, FRG) and added to 100 ml serum bottles containing 20 ml medium described by Nölling et al. (1991). These serum bottles were inoculated with 1 ml of exponentially grown cultures of either strain FF1 or FF3 and incubated for at least two days under  $H_2/CO_2$  at 55°C. Samples of the grown enrichment culture were tested for plaque formation on a lawn of the indicator strains FF1 and FF3.

Table 1. Methanogenic strains used in this study

Strain	Plasmid (size in kb)	Reference
M.thermoformicicum		
Z-245 (DSM 3720)*	pFZ1 (11)	(Zhilina et al., 1984)
FTF (DSM 3012)	pFZ2 (11)	(Touzel et al., 1988)
THF (DSM 3848)	pFV1 (13.5)	(Zinder and Koch, 1984)
CB12 (DSM 3664)	<u>-</u>	(Zhao et al., 1984)
SF-4	-	(Yamamoto et al., 1989)
FF1	_	(Nölling et al., 1991)
FF3	-	(Nölling et al., 1991)
CSM3	-	(Nölling et al., 1993)
HN4	-	(Nölling et al., 1993)
M.thermoautotrophicum		
ΔH (DSM 1053)	_	(Zeikus and Wolfe, 1972)
Marburg (DSM 2133)	pME2001 (4.4)	(Fuchs et al., 1978)

<sup>\*</sup>DSM, German Collection of Microorganisms, Braunschweig, FRG.

# Propagation and titration of phages

For small scale preparation of phage lysates, a single plaque was added to 100 ml serum bottles containing 20 ml medium (Nölling et al., 1991) inoculated with 1 ml of exponentially grown cultures of the appropriate methanogenic host (about 5 x  $10^7$  cells/ml) and incubated for one or two days at 55°C under  $H_2/CO_2$  atmosphere in a shaking incubator at 150 rpm. Large quantities of phage lysate were obtained under similar conditions using 1 l serum bottles containing 0.2 l medium inoculated with 0.2 ml phage lysate (approximately  $10^6$  PFU/ml) and 1 ml of a methanogenic culture. Alternatively, high titer lysates ( $10^9$  PFU/ml) were prepared from plate lysates obtained by flooding agar plates showing confluent lysis with 1.5 ml SM-buffer (Sambrook et al., 1989). For routine propagation of phages, phage lysates were prepared in 100 ml serum bottles as described above, sterilized by filtration through a 0.2  $\mu$ m filter and stored anaerobically at 4°C.

Phage titers were determined by the soft agar overlay method essentially as described by Meile et al. (1989). Usually, 0.1 ml of (diluted) phage lysate was mixed with 0.3 ml exponentially growing cells and incubated for 20 min at room temperature to allow phage adsorption. Soft agar (2.5 ml of 0.7% agar) was added and the mixture was poured onto

freshly prepared and dried Gelrite plates (Nölling et al., 1991). The plates were incubated upside down at 55°C under H<sub>2</sub>/CO<sub>2</sub> atmosphere for one to three days.

# Isolation of DNA

Phage lysates were centrifugated at 10,000 x g for 10 min and the supernatant was collected. DNase and RNase A (Boehringer GmbH, Mannheim, FRG) were added to a final concentration of 0.2 µg/ml, and the supernatant was gently stirred for 1 h at room temperature. Phage particles were precipitated by adjusting the supernatant to 1 M NaCl and 10% (wt/vol) polyethylene glycol 6000, followed by an overnight incubation at 4°C. The phage precipitate was recovered by centrifugation at 10,000 x g for 10 min at 4°C and gently resuspended in SM-buffer. After addition of sodium dodecyl sulfate and EDTA to a final concentration of 0.5% and 20 mM, respectively, the suspension was treated with proteinase K (0.1 mg/ml; Boehringer GmbH, Mannheim, FRG) for 1 h at 56°C. The DNA was deproteinized by several phenol/chloroform extractions followed by an extraction with chloroform. Finally, the DNA was precipitated with ethanol and dissolved in TE buffer (10 mM Tris/HCl pH 8.0, 1 mM EDTA).

Total DNA from strains of the genus *Methanobacterium* was isolated as described by Nölling et al. (1991).

# Manipulation and hybridization of DNA

All restriction enzymes were purchased from Life Technologies Inc. (Gaithersburg, Md.) and used according to the instructions of the supplier. R. MthZI and R. MthTI endonuclease assays were performed as described earlier using extracts prepared from M. thermoformicicum Z-245 (Nölling and de Vos, 1992b) and from E. coli harboring pURM4ΔM with the cloned mthTIR gene from plasmid pFV1 of M. thermoformicicum THF (Nölling and de Vos, 1992a), respectively. To remove histone-like proteins present in the extracts prepared from strain Z-245, R. MthZI assays were deproteinized prior gel electrophoresis as described previously (Nölling and de Vos, 1992b).

For DNA-DNA hybridization, DNA was transferred from agarose gels to Hyperbond membranes by a capillary blot procedure as specified by the supplier (Amersham, United Kingdom). For preparation of DNA probes, either total phage DNA or DNA fragments isolated from agarose gels using the Geneclean kit (Bio 101, La Jolla, Calif.) were labelled by nick-translation (Sambrook et al., 1989) with  $[\alpha^{-32}P]$ dATP (Amersham, United Kingdom). Prehybridization and hybridization were performed as described earlier (Nölling et al., 1991). Washing procedures were carried out in 2 x SSC/0.1% SDS at 55°C (medium stringent) and in 0.1 x SSC/0.1% SDS at 65°C (stringent).

# **Electron microscopy**

Preparations of ΦF1 and ΦF3 were placed on Formvar-coated cooper grids and stained with 1% uranyl acetate. The electron microscope used for examination was a Philips CM12.

# RESULTS

# Morphology of phage ΦF1 and ΦF3

We have previously reported the isolation of the *M.thermoformicicum* strains FF1 and FF3 from an anaerobic, thermophilic digestor (Nölling et al., 1991). Both strains served as indicator for the enrichment and subsequent isolation of two phages from the same anaerobic digestor, which accordingly were designated  $\Phi$ F1 and  $\Phi$ F3.

Electron microscopy of negatively stained phage preparations revealed a similar morphology of both phages  $\Phi F1$  and  $\Phi F3$ . Phage  $\Phi F1$  consists of a isometric, icosahedric capsid approximately 70 nm in diameter and a nonflexible tail of approximately 160 nm in length and 20 nm wide (Fig. 1A). Phage  $\Phi F3$  is composed of a isometric, icosahedric head of approximately 55 nm in diameter and a 230 nm long and 9 nm wide tail which is flexible in contrast to that of phage  $\Phi F1$  (Fig. 1B). The  $\Phi F3$  tail consists of about 60 transversal segments (Fig. 1B). Since no shortened tails were detected, the tails of  $\Phi F1$  and  $\Phi F3$  are probably not contractible. The morphology of both  $\Phi F1$  and  $\Phi F3$  is that of Bradley's classification group B (Bradley, 1967).

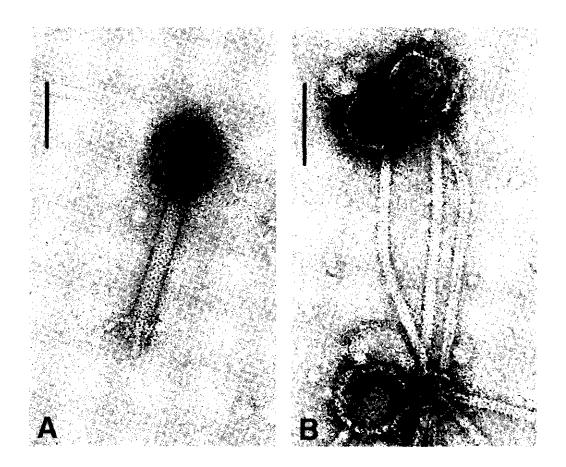


Figure 1. Negatively stained ΦF1 (A) and ΦF3 (B) particles. The bars represent 70 nm.

# Host specificity of phage ΦF1 and ΦF3

All known strains of M. thermoformicicum and the M. thermoautotrophicum strains Marburg and  $\Delta H$  were tested for sensitivity to phages  $\Phi F1$  and  $\Phi F3$ . As summarized in Table 2 both phages differ with respect to their host range. While phage  $\Phi F3$  could only be propagated on M. thermoformicicum FF3, phage  $\Phi F1$  was found to infect a variety of strains including M. thermoformicicum strains Z-245, FFF, FF1, FF3 and CSM3, and M. thermoautotrophicum  $\Delta H$ . No plaque formation was observed when each of the other strains was used as an indicator even not after increasing the number of phages to approximately  $10^5$  PFU per plate.

Table 2. Host range of phage ΦF1 and ΦF3

Strain		ΦF1*	ФF3*
M.thermoformicicum	Z-245	+	
•	FTF	+	_
	THF	-	-
	CSM3	+	_
	FF1	+	-
	FF3	+	+
	CB12	-	-
	SF-4	-	-
	HN4	-	_
M. thermoautotrophicum	ΔΗ	+	-
•	Marburg	-	-

<sup>+,</sup> indicates efficiency of plating of more than 101 while

Lysates produced by  $\Phi F1$  on either host and  $\Phi F3$  lysates contained similar amounts of infective particles and titers of 1-5 x 10<sup>6</sup> PFU/ml were obtained. Phage  $\Phi F1$  formed clear and small (< 1 mm in diameter) plaques that became visible after 2-3 days of incubation. The clear plaques produced by phage  $\Phi F3$  had a size of approximately 2 mm in diameter and could already be detected after about 20 h of incubation. Storing the lysates produced by either phage in the presence of oxygen did not affect the phage titer.

# Genomes of phage ΦF1 and ΦF3

The genome of the phages  $\Phi$ F1 and  $\Phi$ F3 is a double-stranded DNA molecule which served as a good substrate for cleavage by seventeen type II restriction endonucleases with different specificity. For the calculation of the genome sizes and for the construction of physical maps, we have used several commercially available restriction endonucleases and those produced by *M.thermoformicicum* strains THF and Z-245, the GGCC-specific R.*Mth*TI (Nölling and de Vos, 1989a) and the CTAG-recognizing R.*Mth*ZI (Nölling and de Vos, 1989b), respectively.

The size of the  $\Phi$ F1 genome was estimated to be 85  $\pm$  5 kb by summing up the length of

<sup>-,</sup> indicates efficiency of plating of less than 10<sup>5</sup>.

the restriction fragments derived from digestion with SalI (15 fragments; Fig. 2) and a triple digest with XbaI-NotI-MluI (eight fragments). Further restriction analysis revealed no sites for SfI, one site for XbaI and MthZI (Fig. 2) and three sites for MluI (Fig. 2) and NotI. The latter three enzymes were used in double- and triple digestions for the construction of a physical map which showed that  $\Phi F1$  contains a linear genome (Fig. 3). Incubation of  $\Phi F1$  DNA with MthTI generated multiple fragments, the majority of which were smaller than 1 kb (data not shown). To examine whether  $\Phi F1$  contains cohesive ends, MluI-digested phage DNA was heated to  $78^{\circ}C$  for 10 min and immediately cooled on ice. Separation by agarose gel electrophoresis together with non-heated MluI-digested  $\Phi F1$  DNA did not reveal any difference in restriction pattern (data not shown).

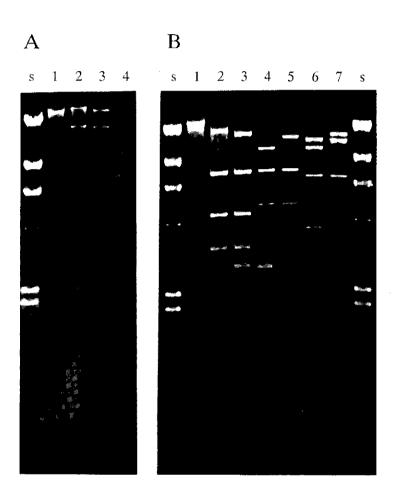


Figure 2. Restriction analysis of DNA prepared from phage ΦF1 (panel A) and  $\Phi$ F3 (panel B). (A) Approximately 0.3 μg ΦF1 DNA undigested (lane 1), and digested with MthZI (lane 2), MluI (lane 3) and SalI (lane 4). (B) Approximately 0.5 μg ΦF3 DNA undigested (lane 1), and digested with SalI (lane 2), Sall-SstI (lane 3), Sall-SstI-MthZI (lane 4). Sall-MthZI (lane 5), SstI-MthZI (lane 6), and MthZI (lane 7), Lanes s show Hind III-digested λ DNA as size marker.

Restriction digestion of phage  $\Phi F3$  DNA with SalI and MthZI produced four and three fragments, respectively (Fig. 2). If the  $\Phi F3$  genome is linear, this would correspond to three SalI- and two MthZI-sites for the  $\Phi F3$  genome which would generate six restriction fragments upon a double digestion with both endonucleases. However, we observed seven fragments derived from digestion of  $\Phi F3$  DNA with SalI followed by incubation with MthZI (Fig. 2).

Interpretation of these results led to the conclusion that phage  $\Phi F3$  contains a circular genome. Mapping of the restriction sites for SstI, HindIII, SalI and MthZI confirmed the circular configuration of the  $\Phi F3$  genome which had a calculated size of  $36 \pm 2$  kb (Fig. 3). The circularization of the  $\Phi F3$  genome seems not to be mediated by cohesive ends since heated (78°C for 10min) and non-heated SalI-digests of  $\Phi F3$  DNA showed no differences in restriction pattern after separation by agarose gel electrophoresis (data not shown).

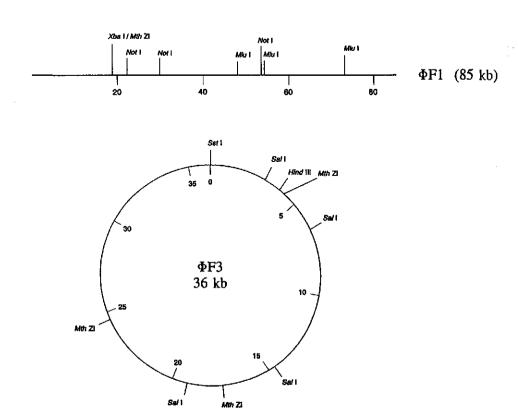


Figure 3. Physical maps of the linear genome of  $\Phi$ F1 and the circular genome of  $\Phi$ F3. Sizes are given in kilobases.

# Homology of ΦF1 and ΦF3 DNA with DNA from other sources

Hybridization studies using radioactively labelled  $\Phi F1$ - and  $\Phi F3$  DNA revealed no similarity to digested total DNA from the *Methanobacterium* strains used in this study (data not shown). In addition, no cross-hybridization was observed between DNA from  $\Phi F1$ ,  $\Phi F3$ ,  $\psi M1$  DNA (data not shown).

Since phage  $\psi M1$  was found to package multimers of plasmid pME2001 harbored by its host *M.thermoautotrophicum* Marburg (Meile et al., 1989), we tested whether phage  $\Phi F1$  contained (fragments of) plasmid pFZ1 DNA from *M.thermoformicicum* Z-245. For this purpose, we extracted DNA from phages propagated on strain Z-245 and the plasmid-free

M.thermoautotrophicum  $\Delta H$  and hybridized it, after digestion and subsequent blotting, to the three cloned KpnI fragments of plasmid pFZ1 labelled by nick-translation (Nölling et al., 1991). The DNA from  $\Phi F1$  phage particles propagated either on strain showed no hybridization with pFZ1 (data not shown) indicating that  $\Phi F1$  does not have the capacity to package pFZ1 DNA.

# DISCUSSION

Two novel lytic phages  $\Phi F1$  and  $\Phi F3$  capable of infecting different thermophilic strains of the archaeal genus *Methanobacterium* were described. Both phages  $\Phi F1$  and  $\Phi F3$  were composed of a polyhedral head and a tail similar to the morphology of the phages found for halophilic and methanogenic *Archaea*, with the exception of the virus-like particle of *Methanococcus voltae* A3 (Wood et al., 1989).

Neither  $\Phi F1$  nor  $\Phi F3$  contained sequences with similarity to DNA from any of the phages or methanogens used in this study. The lack of sequence similarity between  $\Phi F1$ ,  $\Phi F3$  and  $\psi M1$  would imply that these phages use different mechanism to induce lysis of the host cell. Since lysis of *M.thermoautotrophicum* Marburg is mediated by a phage encoded pseudomurein endopeptidase (Stax et al., 1992),  $\Phi F1$  and  $\Phi F3$  may either specify a different lytic activity or induce autolysis of the host.

Phage  $\Phi F1$  contains a linear genome consisting of approximately 85 kb which so far is the largest genome reported for a methanogenic phage. In contrast, DNA extracted from  $\Phi F3$  phage particles was approximately 36 kb in size and showed a circular configuration which is an unusual topology for the genome of a tailed phage. A similar genome topology was, however, found for the virus-like particle from *Methanococcus voltae* A3 which contains a 23-kb DNA molecule (Wood et al., 1989) and the 15.5-kb genome of the virus SSV1 from *Sulfolobus shibatae* (Nadal et al., 1986). The circular form of the  $\Phi F3$  DNA suggests that its genome is either replicated and packaged as a monomer or that replication of  $\Phi F3$  DNA results in a (linear or circular) multimeric form which is resolved into circular monomers during packaging.

The phages  $\Phi F1$  and  $\Phi F3$  differ remarkably in their host range. Similar to phage  $\psi M1$  of M. thermoautotrophicum Marburg, phage PF3 has a narrow host range and could only be propagated on M. thermoformicicum FF3 which served as indicator strain for the isolation of ΦF3. In contrast, phage ΦF1 was capable to infect five strains of M.thermoformicicum and M. thermoautotrophicum  $\Delta H$ . This broad host-range of  $\Phi F1$  is relevant in the context of the phylogenetic studies on thermophilic strains of the Methanobacterium. Based on DNA-DNA similarity (Touzel et al., 1992) and 16S rRNA analysis (Nölling et al., 1993) these studies provided evidence for the conclusion that (i) the species M.thermoformicicum can be divided into two groups of strains, the Z-245- and CB12group, which may constitute different species, (ii) strain M.thermoautotrophicum AH belongs to the Z-245-group, and (iii) M. thermoautotrophicum Marburg is clearly different from either of those strains. The host range of  $\Phi$ F1 that includes *M.thermoformicicum* strains Z-245. FTF, CSM3, FF1 and FF3, and M. thermoautotrophicum  $\Delta H$ , all of which are closely related members of the Z-245-group, supports the proposed different taxonomic position of these thermophilic Methanobacterium strains (Touzel et al., 1992; Nölling et al., 1993).

Phage  $\Phi$ F1 failed, however, to infect *M.thermoformicicum* THF which is a more distantly related member of the Z-245-group (Touzel et al., 1992; Nölling et al., 1993). Although

strain THF could be a trivial phage-resistant mutant it is also possible that the penetrated  $\Phi F1$  DNA is inactivated by endonuclease attack of the plasmid-encoded, GGCC-recognizing type II restriction-modification (R/M) system MthTI of strain THF (Nölling and de Vos, 1992a). If so, the R/M system of strain THF would be more efficient in protecting against phage  $\Phi F1$  infection than the R/M systems MthZI and MthFI of strains Z-245 and FTF, respectively, that are specific for the sequence CTAG (Nölling and de Vos, 1992b). The extreme difference in the frequency of appropriate endonuclease target sites in the 80 kb genome of  $\Phi F1$ , i.e. a single CTAG-site versus multiple GGCC-sites, would support this assumption (Fig. 2 and 3). Although CTAG is one of the rarest occurring tetranucleotides in DNA of methanogens (Nölling, unpublished results) the exceptionally strong bias against CTAG found in the genome of  $\Phi F1$  could well be a result of counterselection against restriction sites in the phage DNA in order to escape the host-controlled restriction barrier. Such an antirestriction mechanism is one of the phage-derived defense strategies known to be realized by certain bacterial bacteriophages to avoid restriction by the host (Krüger and Bickle, 1983).

The specificity of phage  $\Phi F3$  for *M.thermoformicicum* FF3 as only host was unexpected since strain FF3 belongs to the group of closely related strains that serve as host for  $\Phi F1$ . The existence of a type II restriction barrier is not likely since, in contrast to *M.thermoformicicum* strains THF, Z-245 and FTF, extracts prepared from strains FF3, FF1 and CSM3 and *M.thermoautotrophicum*  $\Delta H$  did not contain detectable site-specific endonuclease activities (Nölling and de Vos, 1992b). These findings suggest that phage  $\Phi F3$  depends on a specific factor which is only present in strain FF3 or that the other strains of the Z-245-group contain additional phage defense mechanisms such as type I or III R/M systems.

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Isolation and characterization	of plasmids	from different	strains of	i Methanobacterium
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Journal of General Microbiology 137, 1981-1986.

# Isolation and characterization of plasmids from different strains of Methanobacterium thermoformicicum

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Seven strains of the formate-utilizing thermophilic methanogen Methanobacterium thermoformicicum were screened for the presence of extrachromosomal DNA. Covalently closed circular plasmid DNA was detected in three strains, Z-245, FTF and THF. No plasmids were found in strains CB12 and SF-4, nor in two new isolates, FF1 and FF3. The plasmid from strain Z-245, designated pFZ1, and that from strain FTF, designated pFZ2, were approximately 10-5 kb in size and contained homologous and similarly sized restriction fragments. A physical map of plasmid pFZ1 was constructed and three Kpn1-fragments comprising the entire plasmid were cloned in Escherichia coli using pUC19. Plasmid pFV1 isolated from strain THF was approximately 14 kb in size and contained regions with strong homology to pFZ1 DNA. Using the Methanobacterium formicicum fdhA gene as a hybridization probe the strains of the species M. thermoformicicum could be classified into two major groups.

# Introduction

The concept of the Archae forming one of the three domains of living organisms (Woese et al., 1990) has generated considerable interest in identifying and characterizing archaeal extrachromosomal elements in order to study gene transfer in and develop transformation systems for these unique organisms. Furthermore, detailed knowledge of these extrachromosomal elements contributes to understanding their evolution and their possible interaction with the chromosome of their hosts.

The presence of viruses and virus-like particles has been described in various representatives of the archaeal domain, including sulphur-dependent, halophilic and methanogenic species (for reviews, see Brown et al., 1989; Wood et al., 1989). Several plasmids up to 150 kb in size have been isolated from halophilic bacteria (Brown et al., 1989). Some of these appear to be involved in genome instability (Pfeifer et al., 1981) and carry genes with known functions (DasSarma et al., 1987). In contrast, all plasmids isolated so far from methanogens are cryptic. These include four plasmids derived from Methanococcus (Wood et al., 1985; Zhao et al., 1988), one from Methanosarcina acetivorans (Sowers & Gunsalus, 1988), one from Methanolobus vulcani (Thomm et al., 1983), which also may be a phage (Wilharm et al., 1986), and a plasmid from Methanobacterium thermoautotrophicum strain Marburg (Meile et al., 1983). In this report we describe the isolation of plasmid DNA from three strains of *M. thermoformicicum* and the characterization of one of these plasmids, the cryptic plasmid pFZ1 from strain Z-245. Furthermore, we identify plasmid-free *M. thermoformicicum* strains which may be used as recipient strains in a transformation system.

# Methods

Bacterial strains and vectors. Table 1 lists the strains of M. thermoformicicum used in this study. M. formicicum strain MS1 (DSM 3636) was kindly provided by G. D. Vogels (Department of Microbiology, University of Nijmegen, The Netherlands). M. wolfeit (DSM 2970) and M. thermoautotrophicum strains Marburg (DSM 2133) and AH (DSM 1053) were from the German Collection of Microorganisms, Braunschweig, FRG. Escherichia coli strain DH5\u03c3 and pUC19 (Yanisch-Perron et al., 1985) were obtained from Life Technologies.

Growth conditions. M. formicicum, M. thermoformicicum and M. thermoautotrophicum were grown on minimal medium containing, per litre (J. P. Touzel, personal communication): KH<sub>2</sub>PO<sub>4</sub>, 0 3g; NH<sub>2</sub>Cl, 1-0g; NaCl, 0-6g; MgCl<sub>2</sub>-6ft<sub>2</sub>O, 0-1g; CaCl<sub>2</sub>-2H<sub>2</sub>O, 0-06g; NaHCO<sub>3</sub>, 40g; trace element solution, 10 ml [prepared according to Touzel & Albagnac (1983), except that 0-05 g AlCl<sub>3</sub>-6H<sub>2</sub>O 1-1 was added]. For cultivation in serum bottles 0-5 g cysteine hydrochloride 1-1 was added. The pH of the medium was adjusted to 7-2. For growth of M. wolfei, the medium was supplemented with 2-6 mg Na<sub>2</sub>WO<sub>4</sub>. 2H<sub>2</sub>O 1-1 (Winter et al., 1984). After autoclaving under N<sub>2</sub>/CO<sub>2</sub> (4:1, v/v) the headspace was flushed with 300 kPa H<sub>2</sub>(CO<sub>2</sub> (4:1) and 0-5 g Na<sub>2</sub>S.9H<sub>2</sub>O 1-1 was added. Except for M. formicicum, all methano-

Table 1. M. thermoformicicum strains screened for the presence of plasmid DNA

Strain	Plasmid DNA (size in kb)	Source*
Z-245 (DSM 3720)	pF21 (10-5)	DSM*
FTF (DSM 3012)	pFZ2 (10-5)	DSM
THF (DSM 3848)	pFV1 (14)	DSM
CB12 (DSM 3664)		DSM
SF-4	-	<ul> <li>K. Yamamoto, Osaka</li> <li>City University,</li> <li>Japan</li> </ul>
FFI	_	This work
FF3	_	This work

<sup>\*</sup> DSM, German Collection of Microorganisms, Braunschweig, FRG

genic strains were cultivated according to Schönheit et al. (1980) in 0·8 1 and 10·1 fermenters containing 0·5 1 and 8·1 of medium, respectively. For growth in fermenters Na<sub>2</sub>S was replaced by 0·6·2 g thiosulphate l<sup>-1</sup> and 0·5 g cysteine l<sup>-1</sup> (J. Korteland, personal communication). In addition 10 μg streptomycin ml<sup>-1</sup> was added. Prior to entering the vessel, the gas mixture was led through the gas phase of a closed bottle filled with 100 ml Na<sub>2</sub>S (0·1 g l<sup>-1</sup>) serving as a reducing agent. The cultivation temperature was 37°C for M. formicicum, 55°C for M. thermoformicicum strains Z-245, FTF, CB12, SF-4, FF1 and FF3, and 65°C for M. thermoformicicum strain THF, M. thermoautotrophicum strains Marburg and ΔH and M. wolfei. E. coli strain DH5α was grown in L-broth and handled as described by Maniatis et al. (1982).

Isolation of DNA. Pelleted cells were resuspended in TE buffer (10 mm-Tris/HCI, pH 8-0, 1 mm-EDTA) at a concentration of 1g wet weight in 5 ml buffer. After addition of SDS to a final concentration of 0-5%, proteinase K (0-1 mg ml<sup>-1</sup>; Boehringer Mannheim) and about a one-third volume equivalent of glass beads (0-3 mm), the suspension was incubated for 1 h at 56 °C. After cooling on ice the suspension was vigorously shaken for 15 s on a Vortex mixer and then kept on ice for 15 s. This shaking/cooling procedure was repeated 5-10 times until the cell suspension became viscous. Subsequently, the suspension was thoroughly deproteinized by several phenol/chloroform extractions followed by an extraction with chloroform. Finally, the nucleic acids were precipitated with ethanol and dissolved in TE buffer. In some cases, plasmid DNA was isolated by CsCl/ethidium bromide density-gradient centrifugation (Maniatis et al., 1982).

For copy-number determination of plasmid pFZI, total DNA was isolated from lysed protoplasts of *M. thermoformicicum* strain Z-245 to avoid possible nicking. For this purpose late-exponential phase cells, grown in serum bottles as described above, were harvested and incubated anaerobically with an autolysate of *M. wolfei* until protoplasts were formed, essentially as described by Mountfort et al. (1986). These protoplasts were washed with phosphate/sucrose buffer (Mountfort et al., 1986) and resuspended in ice-cold TE buffer to lyse the protoplasts. The DNA was further purified as described above.

Isolation of formate-utilizing, thermophilic methanogens. Samples were taken from a thermophilic (55 °C) upflow anaerobic sludge-bed reactor (Department of Environmental Engineering, University of Wageningen, The Netherlands) and inoculated into serum bottles containing 20 ml of a selective medium for formate-utilizing methanogens. This consisted of minimal medium as described above with the addition of 50 mM-sodium formate, 50 mM-Tris/HCl, pH 7·3, 0·01 g yeast extract 1-1 and 10 ml vitamin solution 1-1 [prepared according to Balch et al. (1979), except that lipoic acid was omitted]. The cultures were incubated anaerobically at 55 °C under an N<sub>2</sub>/CO<sub>2</sub> atmosphere

(200 kPa overpressure). When the cultures became turbid, samples were plated on selective medium supplemented with 0.62 g thiosulphate 1-1 and 0.5 g cysteine 1-1 instead of Na<sub>2</sub>S and solidified with 0.8% Gelrite (Roth), followed by incubation at 55 °C under an N<sub>2</sub>/CO<sub>2</sub> atmosphere. Colonies became visible after about 1 week and were transferred anaerobically into serum bottles containing selective medium followed by incubation at 55 °C. After growth had developed the cultures were inspected microscopically and methane production was determined with a Becker gas-chromatograph model 417 with a TCD detector. The plating and inoculation procedures were repeated twice for methane-producing cultures.

DNA manipulations. Chromosomal and plasmid DNA were digested with endonucleases obtained from Life Technologies. For cloning into E. coli (Maniatis et al., 1982), DNA fragments of both vector and insert DNA were isolated from agarose gels using a Geneclean kit as described by the supplier (Bio 101). Transfer of DNA from agarose gels to GeneScreen Plus membranes (NEN-Du Pont) was carried out using a capillary blot procedure as described by the supplier. The DNA probe was produced by labelling DNA by nick-translation (Maniatis et al., 1982) with [\alpha^2P]dATP (Amersham). If mixed probes were used, equal amounts of DNA fragments were labelled.

#### Results

Isolation of plasmid DNA and characterization of plasmid pFZ!

Bacteria belonging to the species Methanobacterium have a rigid cell wall, with pseudomurein as the primary component, which is resistant to methods commonly used for lysis of bacterial cells. Therefore, we disrupted the cells by mechanical force using glass beads as has previously been described for the successful disruption of fungal spores (Van Etten & Freer, 1978). Both chromosomal and plasmid DNA from M. thermoautotrophicum strain Marburg (Meile et al., 1983) could be isolated efficiently, which made the method suitable for the rapid screening of methanogens for the presence of plasmid DNA.

Using this procedure, we detected extrachromosomal DNA in *M. thermoformicicum* strain Z-245 (Fig. 1 a, lane 3). To investigate the identity of this DNA, total DNA from strain Z-245 was subjected to CsCl/ethidium bromide density-gradient centrifugation and the covalently closed circular (ccc)-fraction, consisting of supercoiled plasmid, was isolated. Except for some residual chromosomal DNA, the DNA of the ccc-fraction comigrated upon agarose gel electrophoresis with the extrachromosomal DNA band found in the total DNA (Fig. 1a, lanes 3 and 4).

Comparison with supercoiled DNA markers indicated that the plasmid, which was designated pFZ1, had a size of approximately 10.5 kb. A physical map of pFZ1 containing 31 restriction sites was constructed (Fig. 2). Digestion of pFZ1 with *Kpn*I resulted in the formation of three DNA fragments of 2·1, 3·7 and 4·7 kb, fragments I,

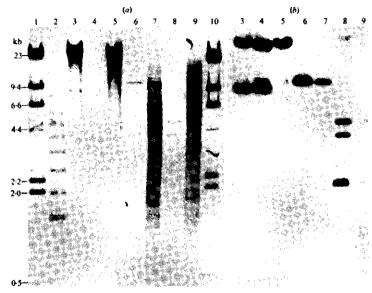


Fig. 1. Agarose gel electrophoresis (a) and Southern hybridization (b) of plasmid pFZ1 DNA purified by CsCl/ethidium bromide density-gradient centrifugation from M. thermoformicicum strain Z-245. Lanes 1 and 10, HindIII-digested phage λ DNA; lane 2, supercoiled size marker (with sizes from top to bottom of 16-2,14-2, 12-1, 10-1, 8-1, 7-0, 6-0, 5-0, 4-0, 3-0 and 2-0 kb) (Life Technologies), lane 3, total undigested DNA of strain Z-245; lanes 4, 6 and 8, coc plasmid DNA fraction, undigested by BamHI and Kpnl, respectively; lanes 5, 7 and 9, oc fraction, undigested, and digested with BamHI and Kpnl, respectively. The autoradiograph (b) is of the corresponding Southern blot hybridized under stringent conditions with equal amounts of Kpnl fragments I, II and III of plasmid pFZ1 labelled by nick-translation. The position of linear DNA size markers (in kb) is shown on the left.

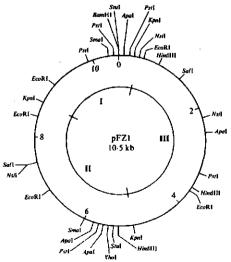


Fig. 2. Restriction map of plasmid pFZ1. The three subcloned KpnI fragments I, II and III that were cloned using pUC19 are indicated in the inner circle. Sizes are given in kb.

II and III respectively (Fig. 2). All three KpnI fragments were cloned in E. coli using pUC19 and used as probe in subsequent hybridization experiments. DNA purified from strain Z-245 by CsCl/ethidium bromide densitygradient centrifugation was digested with BamHI and KpnI, separated by agarose gel electrophoresis, blotted and hybridized to labelled pFZ1 fragments (Fig. 1b, lanes 6-9). Only the expected fragments of plasmid DNA present in the total DNA showed hybridization, indicating that no sequences homologous to plasmid pFZ1 are present in the chromosomal DNA of strain Z-245 (see also Fig. 3). Furthermore, using pFZ1 DNA as probe, no pFZ1 DNA could be detected in the supernatant of a culture of strain Z-245 with methods commonly used for the isolation of bacteriophage DNA (Maniatis et al., 1982; Wood et al., 1989).

We also detected plasmid DNA in M. thermoformicicum strains FTF and THF; these plasmids were designated pFZ2 and pFV1, respectively (Table 1). Plasmid pFZ2 was similar in size to plasmid pFZ1 (10.5 kb, see below). In contrast, plasmid pFV1 was larger than plasmid pFZ1, with a size of approximately 14 kb as revealed by comparison of ccc-DNA from plasmid pFV1 isolated by CsCl centrifugation with supercoiled DNA

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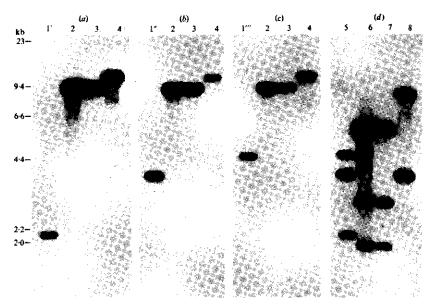


Fig. 3. Southern hybridization of total DNA from M. thermoformicicum strains Z-245, FTF and THF with labelled pFZ1 DNA. Total DNA (about 1-5 µg each) of strains Z-245 (lanes 2 and 6), FTF (lanes 3 and 7) and THF (lanes 4 and 8) was digested with KhoI (panels a, b and c) and HhodIII (panel d) and separated by agarose gel electrophoresis. Blots were hybridized under stringent conditions to equal amounts of KpnI fragments I (a), II (b) and III (c), and to all three fragments (d), labelled by nick-translation. Lanes 1', 1' and 1" contain purified KpnI fragments I, II and III of plasmid pFZ1, respectively, used as the probe; lane 5 contains all three KpnI fragments. The position of linear DNA size markers (in kb) is shown on the left.

markers separated by agarose gel electrophoresis (data not shown). No extrachromosomal DNA was detected in *M. thermoformicicum* strains CB12 and SF-4 or in the new isolates, strains FF1 and FF3.

# Determination of the copy-number of plasmid pFZ1

To determine the copy-number of plasmid pFZ1 several dilutions of total DNA isolated from strain Z-245 were analysed by agarose gel electrophoresis. By comparing the intensity of plasmid and chromosomal DNA bands we found that the intensity of the ccc-plasmid band in the undiluted fraction was comparable with that of the chromosomal DNA band in the fraction diluted 40 times. Assuming that the size of the chromosomal DNA of M. thermoformicicum strain Z-245 is equivalent to that of М. thermoautotrophicum strain Marburg (1.2 × 109 Da) (Brandis et al., 1981), this indicates that strain Z-245 contains at least four copies of pFZ1 per chromosome.

Sequence homologies between plasmid pFZ1 and DNA from other methanogens

None of the labelled KpnI-fragments of pFZ1 (Fig. 2) hybridized to total DNA of M. thermoautotrophicum strains Marburg and ΔH, M. formicicum strain MS1 or M. thermoformicicum strains CB12 and SF-4 and the new isolates FF1 and FF3 (data not shown). In contrast, hybridization of these pFZ1 DNA fragments was observed to total DNA isolated from strains FTF and THF. Subsequent experiments using undigested and digested DNA of both these strains showed that this was due to homology of pFZ1 DNA with the plasmid DNA of strains FTF and THF (data not shown).

To determine the degree of homology between the plasmids, total DNA isolated from *M. thermoformicicum* strains Z-245, FTF and THF was digested with *Xho*I and *HindIII*, separated by agarose gel electrophoresis, blotted and hybridized to the individually labelled *KpnI* fragments I, II and III of pFZ1 (Fig. 2). The results (Fig. 3) indicate that (i) the hybridizing fragments of DNA

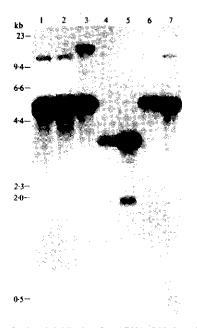


Fig. 4. Southern hybridization of total DNA of M. thermoformicicum with the M. formicicum fdhA gene. Total DNA (about 1.5 µg each) of strains Z-245 (lane 1), FTF (lane 2), THF (lane 3), CB12 (lane 4), SF-4 (lane 5), FF1 (lane 6) and FF3 (lane 7) was digested with BamHI and separated by agarose gel electrophoresis. After transfer to a nyloa membrane, the DNA was hybridized under moderately stringent conditions with a 2-2 kb SphI-BamHI fragment containing the fdhA gene from M. formicicum strain JF-1, labelled by nick-translation (Shuber et al., 1986; kindly provided by J. G. Ferry, Department of Anaerobic Microbiology, VPI, Blacksburg, Va., USA). The position of linear DNA size markers (in kb) is shown on the left.

from strains Z-245 and FTF are of identical size (Fig. 3, lanes 2, 3, 6 and 7), corresponding with that expected from pFZ1 (Fig. 2); (ii) a different hybridization pattern is obtained with DNA from strain THF (Fig. 3, lanes 4 and 8); and (iii) that pFZ1 has no detectable homology with the chromosomal DNA of all three strains.

To analyse the high similarity of plasmid DNA from strains *M. thermoformicicum* Z-245 (pFZ1) and FTF (pFZ2) in more detail, total DNA from both strains was digested with restriction enzymes known to have several recognition sites in plasmid pFZ1 and, after separation and blotting, the DNA was hybridized to labelled pFZ1 DNA. All 31 restriction fragments derived from digestion of plasmid DNA of both strains with *EcoRI*, *PstI*, *ApaI*, *RsaI*, *AluI*, *HaeIII* and *MspI* were found to have the same size (data not shown).

Hybridization of M. thermoformicicum strains to fdhA

As described above M. thermoformicicum strains Z-245, FTF and THF harbour plasmids that are (partially) homologous whereas other strains lack plasmid DNA. Using the M. formicicum fdhA gene as a hybridization probe, the relationship between the M. thermoformicicum strains was examined. As shown in Fig. 4 M. thermoformicicum strains fell into two groups on the basis of hybridization patterns of total DNA: one group, designated the Z-245 group, comprised strains Z-245, FTF and THF (lanes 1, 2 and 3); a second, designated the CB12 group, included strains CB12 and SF-4 (lanes 4 and 5). Within these two groups the hybridization patterns were identical except that strain THF showed a different minor hybridization species (Fig. 4, lane 3).

The fdhA gene was also hybridized to DNA of the new strains FF1 and FF3. These strains were assigned to M. thermoformicicum because of their capacity to produce methane at 55 °C using either  $H_2/\mathrm{CO}_2$  or formate as substrate, and their similar morphology to known M. thermoformicicum strains. The hybridization results (Fig. 4) show that strains FF1 and FF3 seem to be different from each other since the major hybridization species has a slightly different mobility in each case (lanes 6 and 7). Both strains, however, show very similar hybridization patterns that resemble that of strain Z-245, and therefore these new strains may be assigned to the Z-245 group (lanes 2, 6 and 7). Interestingly, both strains FF1 and FF3 lack plasmid DNA, in contrast to all other strains of the Z-245 group (Table 1).

#### Discussion

The present report describes the identification, isolation and characterization of extrachromosomal DNA from the thermophilic, formate-utilizing M. thermoformicicum strains Z-245, FTF and THF. The extrachromosomal DNA of strain Z-245 has the characteristics of plasmid DNA, being isolated in a ccc-form by CsCl/ethidium bromide density-gradient centrifugation and not detectable in the culture supernatant as described for virus-like particles of Methanococcus voltae (Wood et al., 1989). In addition, pFZ1 shows no homology with the chromosomal DNA of the host strain Z-245 nor with that from other species of the genus Methanobacterium tested in this study (Figs 1 and 3). This is, to our knowledge, the first report of the presence of plasmid DNA in formateutilizing, thermophilic methanogens. Plasmid pFZ1 is a relatively low-copy-number plasmid with a minimal four copies per chromosome of strain Z-245 and is stably maintained in its host during several serial transfers in the laboratory. At present we have not been able to assign a specific function to pFZ1, which therefore remains cryptic, as are all other methanogen plasmids described so far.

Hybridization experiments revealed that *M. thermo-formicicum* strains Z-245 and FTF harbour the very similar, if not identical, 10.5 kb plasmids pFZ1 and pFZ2, respectively. Both plasmids are homologous to plasmid pFV1 present in strain THF, which is clearly larger and has a different restriction fragment pattern. These results indicate that the plasmids of *M. thermo-formicicum* share a common ancestor. The presence of highly similar plasmid DNA has been described for *Methanosarcina acetivorans* and two other marine acetorophic strains, all three of which were isolated from the same location (Sowers & Gunsalus, 1988). In contrast, strains Z-245, FTF and THF were isolated from geographically very different locations (Touzel *et al.*, 1988; Zhilina *et al.*, 1984; Zinder & Koch, 1984).

Several attempts have been described to determine the relationship among M. thermoformicicum strains. Yamamoto et al. (1989) suggested that the strains may be divided into two groups, based on the cross-reaction of antibodies raised against strain SF-4 with strain CB12 and Z-245 but not with strain FTF. In contrast, DNA-DNA homology studies (J. P. Touzel, personal communication), indicated that strain FTF is more related to strains Z-245 and THF than to strain CB12 (strain SF-4 was not tested). Our observation that strains Z-245, FTF and THF harbour (partially) homologous plasmid DNA and the results based on the hybridization patterns with the fdhA gene support the classification of strains Z-245, FTF and THF into one group and strains CB12 and SF-4 into another group. On the basis of their hybridization patterns with the fdhA gene the new isolates FF1 and FF3 appear to be related to the Z-245 group. Since they are plasmid-free, those strains could be good candidates as recipients for plasmid pFZ1 or derivatives in transformation studies.

We wish to thank J. P. Touzel for providing strains that were used in an initial stage of the work described here. In addition, we are grateful to K. Yamamoto and G. D. Vogels for providing strains, J. G. Ferry for providing us with the fdh genes and R. Eggen for critical reading of the manuscript.

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Modular organization of related archaeal plasmids encoding different restriction-modification systems in *Methanobacterium thermoformicicum* 

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# Modular organization of related Archaeal plasmids encoding different restriction – modification systems in *Methanobacterium thermoformicicum*

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#### ABSTRACT

Nucleotide sequence comparison of the related 13513-bp plasmid pFV1 and the 11014-bp plasmid pFZ1 from the thermophilic archaeon Methanobacterium thermoformicicum THF and Z-245, respectively, revealed a homologous, approximately 8.2 kb backbone structure that is interrupted by plasmidspecific elements. Various highly conserved palindromic structures and an ORF that could code for a NTP-binding protein were identified within the backbone structure and may be involved in plasmid maintenance and replication. Each plasmid contains at comparable locations a module which specifies components of different restriction - modification (R/M) systems. The R/M module of pFV1 contained, in addition to the genes of the GGCC-recognizing R/M system MthTi, an ORF which may be involved in repair of G-T mismatches generated by deamination of m5C at high temperatures.

# INTRODUCTION

Complete nucleotide sequence analysis of genomes may provide insight into their organization and evolution. In contrast to their bacterial counterparts, only limited information exists on extrachromosomal elements from members of the domain Archaea, a group of prokaryotic organisms that differs fundamentally from Bacteria (1, 2). Nucleotide sequences of only a few extrachromosomal elements isolated from these organisms have been analyzed, including the 15.5-kb genome of the Sulfolobus shibatae virus SSV1 (3), three small plasmids, pHSB1 (1.7 kb), pHGN1 (1.8 kb) and pGRB1 (1.8 kb), isolated from extreme halophilic bacteria (4, 5, 6), and the 4.4-kb pME2001 from the methanogen Methanobacterium thermoautotrophicum strain Marburg (7).

Recently, a family of three related plasmids was identified in the thermophilic archaeon *Methanobacterium thermoformicicum* (8) comprising the nearly identical 11-kb pFZ1 and pFZ2, harbored by strains Z-245 and FTF, respectively, and the closely related 13.5 kb pFV1 of strain THF. In addition to the high

interplasmid similarity, certain plasmids regions were identified with homology to chromosomal DNA from different thermophilic *Methanobacterium* strains that lack plasmid DNA (9). The plasmids may confer a selective advantage to their hosts since it has been shown that restriction and modification (R/M) systems were encoded by pFV1 (10) and pFZ1 and pFZ2 (11).

This report describes the complete nucleotide sequences of pFV1 and pFZ1 and their comparison. Several highly conserved regions were identified that may be involved in replication and maintenance of either plasmid. In addition, a putative DNA-repair enzyme encoded by pFV1 was identified.

#### **MATERIAL AND METHODS**

# Bacterial strains, plasmids and growth conditions

M.thermoformicicum strains THF and Z-245 were cultivated as described previously on  $H_2/CO_2$  as sole carbon and energy source (8). Escherichia coli strains DH5 $\alpha$  (Life Technologies Inc., Gaithersburg, Md.) and TG1 (12) were used for propagation of plasmids pUC18 or pUC19 and phages M13mp18 or M13mp19 (13), respectively, and strain Q359 (14) served as host for propagation of bacteriophage  $\lambda$  GEM-12 (Promega Biotec, Madison, Wis.). All E.coli strains were grown at 37°C in Luria broth-based media (15). If appropriate, ampicillin (50  $\mu$ g/ml), isopropy1- $\beta$ -D-thiogalactopyranoside (1 mM), or 5-bromo-4-chloro-3-indoly1- $\beta$ -D-galactoside (0.004%) was added.

#### Chemicals and enzymes

[\alpha-32P]dATP (110 TBq/mmol) was obtained from Amersham International (Amersham, United Kingdom). All enzymes used for manipulation of nucleic acids were purchased from Life Technologies, Inc. or Pharmacia LKB Biotechnologies (Uppsala, Sweden). Oligonucleotides were synthesized with a Biosearch Cyclone DNA synthesizer (New Brunswick Scientific Corp.) at the Netherlands Institute for Dairy Research (NIZO) or were purchased from Pharmacia (Uppsala, Sweden). Other chemicals were obtained in PA quality from Sigma Chemical Co. (St. Louis, Mo.), from Boehringer GmbH (Mannheim, FRG) or from Merck (Darmstadt, FRG).

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#### DNA isolation and PCR amplification

Total DNA from methanogenic bacteria was isolated as described previously (8). A pFV1 fragment that spans the single XhoI site (position 0/13513) was amplified by PCR as described earlier (16) using total DNA from M.thermoformicicum strain THF and two oligonucleotides, 5'-CTGTAGTTCAGGATC-3' and 5'-GAGATACTGTTCAACTG-3', complementary to positions 377 to 363 and 12921 to 12937 of plasmid pFV1, respectively. The amplification product was treated with Klenow DNA polymerase for 30 min at room temperature in the presence of all four dNTPs (2 mM each), followed by an incubation for 20 min at 55°C in the presence of proteinase K (0.1 mg/ml) and sodium dodecyl sulfate (0.5%) essentially as described by Crowe and coworkers (17). Subsequently, the suspension was extracted with phenol/chloroform, the DNA was precipitated with ethanol. and dissolved in TE buffer (10 mM Tris/HCl pH 8.0, 1 mM EDTA). After digestion of the amplified DNA with HindII and PstI, the 0.4-kb fragment that contained the XhoI-site was recovered from agarose gels using the Geneclean kit (Bio 101, La Jolla, Calif.) and cloned into M13mp19.

#### DNA manipulations and sequence analysis

DNA manipulations were performed essentially as described by Sambrook and coworkers (15). For the determination of the nucleotide sequence, fragments of cloned pFZ1 (8) and pFV1 DNA (see below) were isolated from agarose gels and subcloned into M13mp18/19 vectors. Sequence reactions with vector- or insert specific primers were carried out by the dideoxy chain termination method (18) using either reagents from the Sequenase kit (United States Biochemical Corp., Cleveland, Ohio) according to the recommendations of the manufacturer or reagents for Taqpolymerase sequencing (19). The nucleotide sequence of plasmid pFV1 was determined on both strands apart from two small regions (positions 876–1182 and 2392–2786) that could not be sequenced in both directions due to a premature termination under

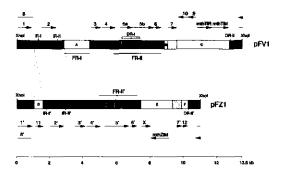


Figure 1. Comparison of the genetic organization of Xhol-linearized pFV1 and pFZ1 from M.thermoformicicum THF and Z-245, respectively. The degree of interplasmid homology is indicated by shading of the maps: the darkly shaded regions show high sequence similarity whereas the white regions A through F represent plasmid-specific sequences. Each ORF listed in Table 1 is shown by a line with an arrowhead indicating its direction. The positions of regions that contain direct (DR) or inverted (IR) repeats are indicated. Dotted lines show positions of fragment insertions. FR-I and FR-II represent regions with homology to chromosomal DNA from several thermophilic strains of the genus Methanobacterium.

all conditions. For plasmid pFZ1 the nucleotide sequence of overlapping fragments was determined on one strand and for 40% on both strands. Computer analysis of sequence data was done with the University of Wisconsin Genetics Computer Group package version 6.0 (20) and the CAOS/CAMM facilities at Nijmegen, The Netherlands.

#### RESULTS AND DISCUSSION

#### Cloning of plasmid pFV1

In a previous report we have shown that *M.thermoformicicum* strain THF harbors the low copy number plasmid pFV1 (8). To be able to analyze this plasmid in detail, covalently closed circular plasmid pFV1 DNA (8) was linearized with *XhoI* and ligated to *XhoI*-digested λ GEM-12. The ligation mix was packaged *in vitro* (15) and used to infect *E. coli* Q359. A 2.3-kb *KpnI*-fragment of plasmid pFZ1 that strongly hybridized to plasmid pFV1 (8), was labelled by nick-translation and used as probe to screen the recombinant phages. A strongly hybridizing recombinant phage, designated λ GFV1, was identified and, after plaque purification, phage DNA was prepared (15). The integrity of the pFV1 insert of λ GFV1 was verified by restriction analysis and hybridization experiments (data not shown). Purified λ GFV1 DNA was used as source of pFV1 DNA in subsequent experiments.

# Nucleotide sequence of plasmid pFV1 and pFZ1 and their comparison

The complete nucleotide sequences of the plasmids pFV1 (EMBL accession number X68366) and pFZ1 (EMBL accession number X68367) from *M.thermoformicicum* strains THF and Z-245, respectively, were determined. The single *Xho*I-site of each plasmids was taken as position 1. Since plasmid pFV1 was originally cloned as a *Xho*I fragment (see above), the uniqueness of this restriction site was confirmed by sequence analysis of a PCR amplified DNA fragment of pFV1 that overlaps the *Xho*I-site. Plasmid pFV1 had a size of 13513 bp and a calculated GC content of 41.8% which is significantly lower than that of its host strain THF (49.6%) (21).

The pFZ1 genome was 11014 bp in length. Alignment of the nucleotide sequences of plasmid pFZ1 and pFV1, schematically shown in Figure 1, revealed a high degree of similarity, confirming previous hybridization experiments (8), and a comparable sequence organization.

Several regions of considerable similarity were identified which are interrupted by plasmid-specific sequences. The homologous sequence blocks, the majority of which shares more than 91% identical nucleotides, add up to approximately 8.2 kb and constitute the backbone structure of both plasmids (Figure 1). As a consequence, these regions have comparable coding capacities and may specify proteins with more than 84% identical amino acids (Table 1).

Two plasmid regions, designated FR-I and FR-II (Figure 1), were found to have homologous counterparts in the chromosomal DNA of several thermophilic *M.thermoformicicum* strains that lack plasmid DNA (9). FR-I resembles an insertion sequence (9) and is specific for plasmid pFV1 (see below), whereas FR-II is part of both plasmids. FR-II of pFV1, however, contains a direct repeat of two identical 524-bp sequences (DR-I, position 6374 to 7421; Figure 1) that is not found in the corresponding region of plasmid pFZ1.

The most conspicuous difference between the plasmids pFV1 and pFZ1 is the presence of three unique sequences that could

be identified in each plasmid (element A-F in Figure 1). The location of two of those elements, A and D, in regions with high interplasmid similarity allowed to determine their exact size. The AT-rich element A (GC content 29.7%), which corresponds to FR-I (Figure 1), is located on plasmid pFV1 (position 2852 to 4352) and comprises 1501 bp. Element D is a 569-bp insertion of plasmid pFZ1 (position 917 to 1485; Figure 1) and contains open reading frame (ORF) 11 (Figure 1). Four other unique sequences, B and C of plasmid pFV1 and E and F of plasmid pFZ1, are located at similar positions relative to the plasmid backbone and flank a region of approximately 0.5 kb that exhibits only relatively low interplasmid similarity (69%; Figure 1). The two large plasmid-specific elements C and E of pFV1 and pFZ1, respectively, code for components of recently characterized R/M systems: the GGCC-recognizing MthTI system of plasmid pFV1 comprising the methyltransferase (MTase) gene mthTIM and the endonuclease (ENase) gene mthTIR (10), and the CTAGrecognizing system MthZI of plasmid pFZ1 encoded by the MTase gene mthZIM and ORF X which may code for the corresponding ENase (11) (Figure 1). Moreover, two additional ORFs, ORF9 and 10, are located on the unique pFV1-fragment C in close proximity to the genes of the MthTI system, one of which, ORF10, may encode a protein with considerable similarity to enzymes involved in DNA mismatch repair (see below).

#### Repeated sequences of plasmid pFV1 and pFZ1

The close relationship of pFV1 and pFZ1 (Figure 1) implies a similar replication mechanism for both replicons that should be specified by the conserved backbone structures. Since repeated sequences are known to be involved in the replication of bacterial plasmids (for reviews: 22, 23), we searched in the nucleotide sequence of pFV1 and pFZ1 for regions that contain direct (DR) or inverted repeats (IR).

Apart from DR-I of plasmid pFV1 described above, a region with several DRs was identified in the backbone structure of both plasmids (Figures 1). This 490-bp segment of plasmid pFV1 (DR-II; position 12681 to 13170) contains three perfect 51-bp and two nearly perfect 33-bp repeats. Comparison with the corresponding region of plasmid pFZ1 (DR-II', position 10265 to 10671) showed, however, only limited similarity, and only the two 33-bp repeats were found to be almost completely conserved.

Inspection of the pFV1 and pFZ1 nucleotide sequences revealed two IRs, IR-I and IR-II, that are contained within highly conserved, non-coding regions of both plasmids (Figure 1). Both IR-I and IR-II exhibit a high GC-content of 52% GC and 62% GC, respectively, and have the capacity to form secondary structures. In IR-I (position 1102 to 1419 in pFV1; Figures 1 and 2), four potential hairpin structures (IR1-IR4, Figure 2) could be identified. Remarkably, the hairpin loops formed by IR1 and IR4 contain a partially overlapping pentamer with the sequence 5'-TCGCT which is repeated four times in the loop of IR1 and five times in the loop of IR4 (Figure 2).

The second region with palindromic sequences, IR-II, is located approximately 1 kb downstream of IR-I (ranging from position 2392 to 2593 in plasmid pFV1) and contains two palindromic sequences, IR5 and IR6 (Figure 2). Analogous to IR-I, two partially overlapping repeats of the pentamer TCGCT are present in both the hairpin loop and the stem/interior loop of IR6, whereas perfect repeats of this pentamer are also found in the region between IR5 and IR6 (Figures 1 and 2).

Both IR-I and IR-II represent one of the most conserved plasmid regions in pFV1 and pFZ1 that differ at only 11 positions out of 520 nucleotides (Figure 2). This high conservation of the IR-regions may indicate an essential function in plasmid maintenance or replication functions. Interestingly, in plasmids that replicate by a rolling circle mechanism via a single-stranded intermediate, (imperfect) palindromic structures are part of the so-called plus and minus origin, the former of which is used for initiation of replication by a plasmid-encoded Rep protein (22). Moreover, the hairpin loops of the minus origins were found to share the consensus sequence 5'-TAGCGT (24). This sequence resembles the complementary sequence of the repeated pentamer 5'-TCGCT which has been observed in hairpin loops of IR-I and IR-II of both plasmids pFV1 and pFZ1. However, we neither could detect single-stranded pFV1- or pFZ1 DNA in hybridization experiments (data not shown) nor found similarity of any of the plasmid-backbone encoded proteins with conserved sequence motifs of rolling circle replication initiator proteins (25). Therefore, the involvement of the IR-regions in replication remains to be confirmed.

# Coding capacity and putative genes of plasmid pFV1 and pFZ1 $\,$

Analysis of the nucleotide sequences of plasmid pFV1 and pFZ1 for coding regions revealed 13 and 12 ORFs, respectively, that could code for polypeptides composed of more than 100 amino

Table 1. Comparison of (putative) genes located on plasmids pFV1 and pFZ1

Gene	plasmid pFV1				plasmid pFZ1			- %
	Amino acids	Start codon	DNA sequence	- Gene	Amino acids	Start codon	DNA sequence	Identity
ORFI	364	ATG	13304 - 882	ORFI'	364	ATG	10805 - 882	99
ORF2	284	ATG	1511-2362	ORF2'	284	ATG	2101-2952	85
ORF3	197	ATG	4438 - 5028	ORF3'	217	ATG	3455-4105	98
ORF4	237	ATG	5152-5862	ORF4'	234	ATG	4225 - 4926	91
ORF5a	227	ATG	6229-6909	ORF5'	499	ATG	5295-6791	72
ORF5b	451	GTG	6912 - 8264	ORF5'	499	ATG	5295-6791	84
ORF6	122	ATG	8354 - 8719	ORF6'	122	ATG	6894 - 7259	98
ORF7	145	ATG	9186 9620	ORF7'	80	ATG	9647 - 9886	71
ORF8	361	ATG	822-13253	ORF8'	361	ATG	822-10754	88
ORF9	146	ATG	10733 - 10296	ORF11	148	ATG	1093 - 1536	-
ORF10	221	TTG	10300-9638	ORF12	117	GTG	9889 - 10239	-
mthTIR	281	ATG	10827 - 11669	ORFX	202	GTG	7539 - 8144	_
mthTIM	330	ATG	11669 12658	mthZIM	355	ATG	9203 - 8139	_

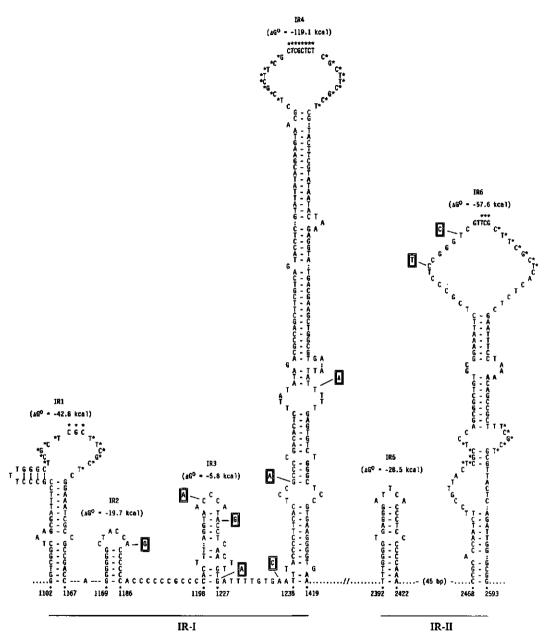


Figure 2. Potential secondary structures of regions IR-I and IR-II and their locations in pFV1. The free energy ( $\Delta G^{\circ}$ ) values of the potential hairpin loops IR! to IR6 were calculated using the PCGENE program RNAFOLD. Nucleotides different with the corresponding regions of pFZ1 are indicated. The repeated pentamers 5'-TCGCT are marked by asterisks.

acids (Figure 1; Table 1). Except for ORF8 of pFV1 and the homologous ORF8' of pFZ1, all ORFs located in the backbone structure have the same orientation. Each plasmid specifies components of different R/M systems (10, 11) which are encoded by genes located on the plasmid specific elements C (pFV1) and E (pFZ1) (Figure 1). The deduced amino acid sequences of the other ORFs of pFV1 and pFZ1, listed in Table 1, were analyzed for similarity with sequences present in the SwissProt data base (release 22.0).

The homology search showed that ORF1 of plasmid pFV1 and its counterpart ORF1' of plasmid pFZ1 contain a stretch of amino acids with similarity to the purine nucleotide binding site of ATP-or GTP-utilizing proteins (Table 2). This NTP-binding site is formed by a characteristic amino acid motif (NTP-motif) composed of two elements A and B (26, 27) and—analogous to several NTP-binding enzymes involved in DNA-metabolism (27-30)—is located within the N-terminal part of the ORF1 and ORF1' proteins (Table 2). Together with the high conservation

Table 2. Alignment of the NTP-motif containing domain of ORF1 with NTPbinding proteins involved in DNA metabolism. Identical or similar residues are boxed.

Protein	Sequence A	Sequence B	Reference
RecD 166 UVID 24 RUVB 57 ORF1 63	SV I S G CP G T CKT TYVAKL L -7. LL V L A GA G S CKT RVLVKR I -1. LL I V G PP G L GKT TLANIV A -3 LL I V G PP G S GKT VTKYV I -5		

of the deduced ORF1 and ORF1' proteins (>99% identical residues; Table 1), the presence and location of this NTP-binding motif strongly suggests that both proteins are involved in the replication of pFV1 and pFZ1. Transcription and translation of ORF1 and ORF1' may be initiated at sequence motifs that were found preceding the coding regions. A sequence stretch with similarity to a typical archaeal promoter signal (31, 32) was identified ranging from position 13228 to 13258 in pFV1 and from position 10729 to 10759 in pFZ1. The first translation initiation codon (ATG) is preceded by a sequence with similarity to a consensus methanogenic ribosome binding site (33), ranging from position 13294 to 13300 in pFV1 and from position 10795 to 10801 in pFZ1. However, no sequences resembling the consensus archaeal terminator signal (33) have been recognized downstream of ORF1 and ORF1'.

Within the pFV1-specific DNA element C which contains the genes for the MthTI R/M system, two other ORFs, designated ORF9 and ORF10, were identified that could code for proteins of 146 and 221 amino acids, respectively (Figure 1; Table 1). A database search revealed that the protein deduced from ORF10 shares significant sequence similarity with two E.coli proteins, MutY and endonuclease III (52.4% and 50.0% similarity and 28.8% and 28.4% identity), respectively, which are known to be involved in DNA mismatch repair. MutY and endonuclease III, composed of 350 (34) and 211 amino acids (35), respectively, both possess N-glycosylase activity as well as apurinic/apyrimidinic (AP) endonuclease activity (36–39). They differ, however, in their substrate specificity. While MutY is involved in the correction of A/G (35), A/C (37) and A/8-oxoG

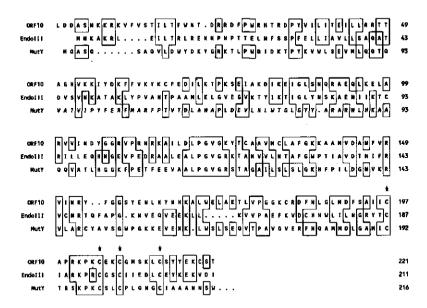


Figure 3. Amino acid sequence alignment of the putative ORF10 protein of pFV1 with endonuclease III and MutY of E.coli. Identical amino acids are boxed. Dots represent gaps that have been introduced to optimize the alignment. Positions marked with asterisks represent the four highly conserved cysteine residues. Numbers at the right refer to amino acid residues.

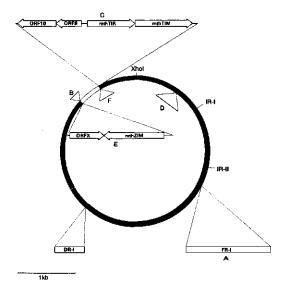


Figure 4. Schematic representation of the conserved 8.2 kb backbone structure obtained from nucleotide sequence alignment of pFV1 and pFZ1. Insertions indicated outside the circle represent pFV1-specific sequences, those inside are specific for pFZ1 (the bar represents a size of 1 kb).

mismatches (8-oxoG = 8-hydroxyguanine) (40), endonuclease III is active on mismatches generated by certain derivatives of thymidine and cytosine (38, 39). Alignment of the deduced amino acid sequences of the ORF10 protein, endonuclease III and MutY (Figure 3) revealed (i) a highly conserved motif LPGVG(R/K)XT (position 120 to 127 of the ORF10 protein; X=variable amino acid), and (ii) a stretch of four cysteine residues spaced by an identical number of amino acids (CX6CX2CX5C), which is located at corresponding positions in the three polypeptides. Since endonuclease III was shown to be an iron-sulfur protein (41), those cysteine residues are believed to be involved in the [4Fe-4S]<sup>2+</sup> cluster binding (41). It therefore seems to be likely that MutY, as already suggested by Michaels and coworkers (34), and the putative ORF10 protein specified by plasmid pFV1 are iron-sulfur proteins with [4Fe-4S]2+ clusters. The observed sequence similarities suggest that the ORF10 protein acts, like MutY and endonuclease III, as a DNA repair enzyme that recognizes incorrect base pairing.

The presence of such a repair system in the thermophilic *M.thermoformicicum* strain THF is plausible since the pFV1-encoded GGCC-recognizing methyltransferase *M.Mth*TI generates 5-methylcytosine (m<sup>5</sup>C) (10) which is, especially under thermophilic conditions, subject to deamination (m<sup>5</sup>C T) resulting in a G-T mismatch (42). To avoid the probably lethal effect of multiple transitions, strain THF should contain a mechanism that either prevents deamination of m<sup>5</sup>C or is capable to correct the G-T mismatches. The pFV1-encoded ORF10 protein is a good candidate to act as a G-T mismatch repair enzyme in *M.thermoformicicum* THF. Moreover, the close proximity of ORF10 and the *Mth*TI system would support a functional relation of the endonuclease, the methyltransferase and

the putative DNA mismatch repair enzyme. Such a clustering may also facilitate the simultaneous transfer of these genes between cells and ensures the coordinate activity of the encoded enzymes in the recipient which probably is necessary for its survival. Interestingly, a similar genetic linkage has been found for the functionally related methyltransferase and DNA mismatch repair enzyme in the *dcm-vsr* system of *E.coli* (42).

It seems paradoxical that M. thermoformicicum THF maintains a non-chromosomally encoded R/M system with a m5Cproducing MTase activity and, as a consequence, a DNA mismatch repair enzyme. A possible explanation is that, under thermophilic conditions, a combination of the enzymes specified by the GGCC-recognizing MthTI R/M system and ORF10 may serve as a protection mechanism against infection by phages that exhibit the same methylation pattern as produced by the MTase M.MthTI, i.e. GGmeCC. Such phages may have escaped the restriction barrier of strain THF or have acquired a protecting MTase gene. Since their methylated DNA is resistant against digestion by the host-encoded ENase, such phages normally would be able to infect the entire population. However, as a result of elevated deamination of m5C at high temperatures without mispair correction, the genome of those phage particles accumulate, in contrast to the host genome, partially and fully dearninated GGmeCC-sites the latter of which would result in two juxtaposed G-T mismatches per site. One may envisage several scenarios once this phage DNA has entered the host cell. Firstly, the ORF10 protein could be unable to initiate mispair correction at juxtaposed G-T mismatches which may decrease the infectivity of the damaged phage DNA. The second scenario is based on the observation that the mutHLS-dependent mismatch repair systems of certain E. coli mutants produce double-strand breaks due to initiation of mismatch correction along with an endonucleolytic attack on either DNA strand (44, 45). Doublestrand breaks in the deaminated phage DNA may be generated during initiation of mismatch correction by the putative ORF10 protein which - analogous to MutY and endonuclease III - may act as N-glycosylase and AP-endonuclease on the opposite strands of the juxtaposed G-T mismatch base pairs. This would generate a double-stranded break 3' from the GG-dinucleotide of the GGCC site resulting in a similar effect as restriction of the unmethylated phage DNA by the ENase of the R/M system MthTI.

#### CONCLUSION

Sequence analysis of the plasmids pFV1 and pFZ1 from the archaeon *M.thermoformicicum* strain THF and Z-245, respectively, has confirmed their close relationship. Both plasmids display a modular genome organization and consist of a highly conserved, approximately 8.2 kb backbone which is interspersed with plasmid-specific, accessory elements of variable size and function (Figure 4).

The high sequence similarity and comparable genetic maps of the plasmids pFV1 and pFZ1 indicate either the presence of a common ancestor or that one of the plasmids originated from the other. In either case, accessory elements have been acquired or lost.

The conserved backbone structure is expected to specify function necessary for plasmid replication and maintenance. These essential plasmid functions may include two regions, IR-I and IR-II (Figures 2 and 4), with the capacity to form highly conserved secondary structures, and, in close proximity to those

IR-regions, ORF1 that could encode a protein with NTP-binding activity (Figure 1. Table 2).

While the nature of the smaller elements specific for pFV1 and nFZ1 remains unknown, element A of plasmid pFV1, which corresponds to FR-L has various features of an insertion sequence (9). In addition, each plasmid contains, analogous to the functional modules observed for lambdoid phages (46), at comparable locations an element which specifies components of a R/M system recognizing either the sequence GGCC (pFV1) (10) or CTAG (nFZ1) (11). Within the R/M module of plasmid pFV1, two additional ORFs were identified, one of which, ORF10, may code for a DNA-repair enzyme that is functionally related to the GGCC-recognizing R/M genes.

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Distribution and characterization of plasmid-related sequences in the chromosomal DNA of different thermophilic *Methanobacterium* strains

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# SUMMARY

The genomes of several thermophilic members of the genus Methanobacterium were analyzed for homology to the related restriction-modification plasmids pFV1 and pFZ1 from M.thermoformicicum strains THF and Z-245, respectively. Two plasmid-located regions, designated FR-I and FR-II, could be identified with chromosomal counterparts in six Methanobacterium strains. Multiple copies of the pFV1-specific element FR-I were detected in the M.thermoformicicum strains CSM3, FF1, FF3 and M.thermoautotrophicum  $\Delta H$ . Sequence analysis showed that one FR-I element had been integrated in an almost identical sequence context in the chromosomes of the strains CSM3 and  $\Delta H$ . Comparison of the FR-I elements from these strains with the one from pFV1 revealed that they consisted of two subfragments, boxI (1118 bp) and boxII (383 bp), with a variable sequential order. Each subfragment was identical on the sequence level with the corresponding one of either FR-I element and was flanked by terminal direct repeats with the consensus sequence A(A/T)ATTT. These results suggest that FR-I represents a mobile element. FR-II was located on both plasmids pFV1 and pFZ1, and on the chromosome of M. thermoformicicum strains THF, CSM3 and HN4. Comparison of the nucleotide sequences of the two plasmidlocated FR-II copies and the one from the chromosome of strain CSM3 showed that the FR-II segments were approximately 2.5-3.0 kb in size and contained large ORFs that may encode highly related proteins with a yet unknown function.

#### INTRODUCTION

Genomic rearrangements and mobilization of genetic material are evolutionary processes of prokaryotic and eukaryotic cells that for a part are induced by transposable elements, i.e. insertion sequences (IS) and transposons, due to their ability to move within or between genomes. These mobile elements are also known to be involved in controlling gene expression by providing signals that may enhance or suppress transcription of genes. Being studied in depth within the *Bacteria* (for reviews see: Berg and Howe 1989; Graig and Kleckner 1987), mobile elements have also been described in *Archaea*, a group of phylogenetically related prokaryotes with distinct biochemical and genetic properties (Woese et al. 1990; Zillig 1991)

A variety of diverse IS elements have been characterized in halophilic Archaea, one of the three major archaeal groups, and found to be located on plasmids (DasSarma et al. 1983; Pfeifer et al. 1983; Ebert et al. 1984), phages (Schnabel et al. 1984) or chromosomal DNA

(Pfeifer 1986; Hofman et al. 1986). Movement of those transposable elements resulted in a high frequency of DNA-rearrangements causing genome instability in certain halobacteria (Pfeifer et al. 1981; Sapienza et al. 1982). In contrast, among the other two archaeal groups, the sulfur-dependent and the methanogenic organisms, only one IS element, ISM1, was identified in the chromosome of the mesophilic *Methanobrevibacter smithii* (Hamilton and Reeve 1985).

In a previous report we described the isolation of plasmids from several strains of the thermophilic archaeon *Methanobacterium thermoformicicum* (Nölling et al. 1991). The well-characterized low copy number plasmid pFZ1 of strain Z-245 was found to be highly homologous, if not identical to plasmid pFZ2 of strain FTF and partially homologous to plasmid pFV1 from strain THF indicating a close relationship and a common origin of these plasmids. Sequence comparison of pFV1 and pFZ1 revealed a modular genome organization consisting of a highly conserved backbone structure that is interspersed with plasmid-specific elements (Nölling et al. 1992). Two of these elements specify components of restriction-modification (R/M) systems, the GGCC-recognizing *Mth*TI system of pFV1 (Nölling and de Vos 1992a) and the CTAG-specific *Mth*ZI system carried by pFZ1 (Nölling and de Vos 1992b).

A pFV1-specific element and a region within the conserved backbone structure of both plasmids were found to have homologous counterparts located on the chromosome of several thermophilic, plasmid-free strains of the genus *Methanobacterium*. The analysis of those two homologous regions, described in the present report, showed that at least one shares some structural similarities with IS elements identified in *Bacteria* and other *Archaea*.

# **METHODS**

# Bacterial strains and growth conditions

Strains of the genus *Methanobacterium* and *Escherichia coli*, bacteriophages and plasmids used in this study are listed in Table 1. All methanogenic strains were grown as described earlier (Nölling et al. 1991). *E.coli* cultures were cultivated at 37°C in L-broth, if appropriate in the presence of ampicillin (50  $\mu$ g/ml), and handled as described by Sambrook et al. (1989).

# DNA techniques and plasmid constructions

DNA from methanogenic bacteria was isolated with the glass-bead method as described by Nölling et al. (1991). Digestion of chromosomal and plasmid DNA with restriction endonucleases, cloning of DNA fragments, ligation of DNA, transformation of plasmid DNA into *E.coli*, handling of M13 phages and isolation of double and single stranded DNA from M13 phages was carried out essentially as described by Sambrook et al. (1989). DNA of both vector and insert DNA was isolated from agarose gels and purified by the Geneclean procedure (Bio 101, La Jolla, Calif.).

All restriction endonucleases and other DNA-modifying enzymes were obtained from Life Technologies. Oligonucleotides were synthesized with a Biosearch Cyclone DNA synthesizer (New Brunswick Scientific Corp.) at the Netherlands Institute for Dairy Research (NIZO).

All recombinant plasmids were constructed in E.coli as described in Table 1. Plasmid

Table 1. Bacterial strains and plasmids used in this study

Strain or plasmid	Property or genotype	Source or reference			
M.thermoformicicum					
THF	Harbors plasmid pFV1 (13.5 kb)	DSM3848*; (Zinder and Koch, 1984)			
Z-245	Harbors plasmid pFZ1 (11.0 kb)	DSM 3720; (Zhilina and Ilanionov, 1984)			
FTF	Harbors plasmid pFZ2 (11.0 kb)	DSM 3012; (Touzel et al., 1988)			
FF1, FF3, CSM3, HN4	Plasmid-free	(Nölling et al., 1991, 1993)			
SF-4	Plasmid-free	(Yamamoto et al., 1989)			
CB12	Plasmid-free	DSM 3664; (Zhao et al., 1986)			
M.thermoautotrophicum					
ΔH	Plasmid-free	DSM 1053; (Zeikusand Wolfe, 1972)			
Marburg	Harbors plasmid pME2001 (4.4 kb)	DSM 2133; (Fuchs et al., 1978)			
E.coli					
DH5α	F lacZΔM15 recA1 hsdR17 supE44 Δ(lacZYA-argF)	Life Technologies			
TG1	F[traD36 proAB <sup>+</sup> lacP lacZΔM15] supE hsdΔ5 Δ(lacproAB)	(Gibson, 1984)			
Plasmids					
pUC18/pUC19	Ap <sup>r</sup>	(Yanisch-Perron et al., 1985)			
pUV1	7.4 kb Sstl-Xhol fragment of pFV1 in pUC19 Sstl-Sall, Ap	(Nölling and de Vos, 1992)			
pUV2	6.1 kb Sstl-Xhol fragment of pFV1 in pUC19 Sstl-Sall, Ap	(Nölling and de Vos, 1992)			
pUV7	1.5 kb Acci(blunt end)-Nsil fragment of pUV1 in pUC19 KpnI(blunt end)-Psil, Ap	This study			
pUΔH1	4.0 kb EcoRI fragment from M.thermoautotrophicum ΔH in pUC19, Ap	This study			
ρUΔΗ2	1.7 kb Scal-Pstl fragment from strain ΔH in pUC19 Smal-Pstl, Ap	This study			
pUCM1	1.4 kb EcoRI fragment from M.thermoformicicum CSM3 in pUC19, Apr	This study			
pUCM2	1.2 kb EcoRI fragment from strain CSM3 in pUC19, Apr	This study			
pUCM3	1.6 kb Scal-Pstl fragment from strain CSM3 in pUC18 Smal-Pstl, Ap	This study			
pUCM4	1.8 kb EcoRI fragment from strain CSM3 in pUC19, Apr	This study			
pUCM5	1.0 kb fragment amplified from total DNA of strain CSM3 DNA by PCR and cloned into pUC19 HindII, Apr	This study			
pUCM6	4.5 kb EcoRI fragment from strain CSM3 in pUC19, Apr	This study			

DSM, German Collection of Microorganisms, Braunschweig, FRG.

pUV7 was constructed by cloning a 2.3-kb NsiI-KpnI fragment of pUV1 into pUC19 digested with PstI and KpnI followed by deletion of a 0.8-kb AccI-KpnI fragment, filling up the ends with Klenow polymerase and religation.

# PCR amplification

PCR conditions applied for amplification of a chromosomal fragment were essentially as described earlier (Nölling et al. 1993) using total DNA from M.thermoformicicum CSM3 and two oligomers, 5'-CATTTTCACATCTCC and 5'-GTCCTACTGCTTTCAC, complementary to positions 600 to 586 and 1057 to 1072, respectively, of FR-Ic from strain CSM3. The amplified DNA was treated for 30 min at room temperature with Klenow DNA polymerase in the presence of all four dNTPs (2 mM each), followed by an incubation with proteinase K (0.1 mg/ml; Boehringer Mannheim, FRG) and sodium dodecyl sulfate (0.5%) for 20 min at 55°C essentially as reported by Crowe and coworkers (1991). Subsequently, the suspension was subjected to several phenol/chloroform extractions and the DNA was precipitated with ethanol and finally dissolved in TE buffer (Sambrook et al. 1989).

## Southern hybridization

DNA was transferred from agarose gels to GeneScreen Plus nylon membranes (NEN-DuPont) by the capillary blot procedure (Sambrook et al. 1989). Hybridization and washing of the filters was carried out according to the membrane manufacturer's protocol. Labelled DNA probes were produced by nick-translation (Sambrook et al. 1989) with  $[\alpha^{-32}P]dATP$  (110 TBq/mmol; Amersham). A 1.1-kb *EcoRI* fragment of the pUV7 insert was used to probe for sequences homologous to FR-I (Fig. 1). The FR-II-specific probe consisted of equal amounts of the 2.1-kb *NarI-SsI* fragment of pUV1 and the 1.2-kb *SsI-EcoRI* fragment of pUV2 (Fig. 1).

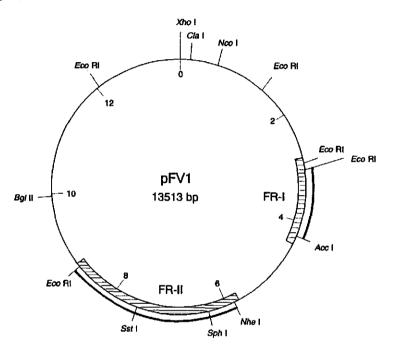


Figure 1. Physical map of plasmid pFV1 from *M.thermoformicicum* THF. Coordinates were taken from Nölling et al. (1993). The regions with homology to the chromosome of other *Methanobacterium* strains, FR-I and FR-II, are indicated by open boxes. The fragments of pFV1 used as FR-I- and FR-II-specific probes are marked by a black bar. Only restriction sites relevant for this study are shown.

## Sequence analysis

DNA sequencing was performed by the dideoxy chain termination method (Sanger et al. 1977) with a Sequenase kit (United States Biochemical Corp., Cleveland, Ohio) according to the manufacturer's recommendations, using single stranded DNA prepared from M13mp18/19-based clones (Yanisch-Perron et al. 1985) and vector- and insert-specific primers. Computer analysis of the sequence data was done with the PC/GENE version 5.01 (Genofit, Geneva, Switzerland) while the GCG package version 6.0 (Devereux et al. 1984)

was used to screen the GenBank (release 72.0) and the SwissProt (release 23.0) databases present at the CAOS/CAMM facilities in Nijmegen, The Netherlands.

## RESULTS

# Sequence homology between plasmid pFV1 and DNA from other methanogens

Total DNA prepared from strains of *M. thermoformicicum* and *M. thermoautotrophicum* were screened for the presence of sequences homologous to plasmid pFV1 from *M. thermoformicicum* THF. In initial hybridization experiments the *SstI-XhoI* inserts of plasmids pUV1 and pUV2 were used as probes (Fig. 1, Table 1). Positive hybridization signals were found under stringent conditions with total DNA isolated from *M. thermoformicicum* strains THF, Z-245, FTF, FF1, FF3, CSM3 and HN4 and with

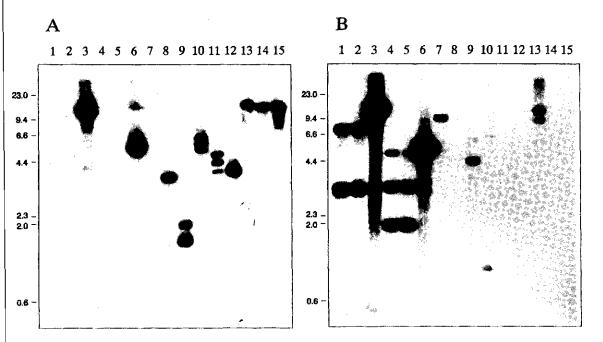


Figure 2. Southern hybridization of total DNA from thermophilic Methanobacterium strains with radioactively labelled probes for FR-I (panel A) and FR-II (panel B). Total DNA (about 0.5 μg each) of M.thermoformicicum strains Z-245 (lanes 1, 4), FTF (lanes 2, 5), THF (lanes 3, 6), HN4 (lane 7), CSM3 (lanes 9, 10, 13), FF1 (lanes 11, 14) and FF3 (lanes 12, 15), and M.thermoautotrophicum ΔH (lane 8) was digested with SphI (lanes 1-3), EcoRI (lanes 4-9), BamHI-PstI (lanes 10-12) and SalI-SphI (lanes 13-15), and fractionated by gel electrophoresis on a 0.7% agarose gel. After transfer to a nylon membrane the blots were hybridized under stringent conditions with a 1.1-kb EcoRI-AccI fragment of pFV1 (FR-I-specific probe; panel A) and a 3.3-kb NarI-EcoRI fragment of pFV1 represented by a 2.1-kb NarI-SstI fragment of pUV1 and a 1.2-kb SstI-EcoRI fragment of pUV2 (FR-II-specific probe; panel B). Numbers to the left refer to HindIII fragments of λ DNA (in kb) used as size marker.

M.thermoautotrophicum ΔH (Fig. 2), whereas no hybridization was observed with total DNA isolated from M.thermoformicicum strains CB12 and SF-4 and M.thermoautotrophicum Marburg (not shown). In order to define those homologous regions a series of hybridization experiments was carried out using subfragments of cloned pFV1 DNA as probe. Two distinct regions of plasmid pFV1, designated FR-I (fragment I) and FR-II (fragment II) (see below), were identified that hybridized with DNA from thermophilic Methanobacterium strains (Fig. 1; Table 2). The FR-I specific probe showed hybridization with DNA from M.thermoformicicum strains CSM3, FF1 and FF3 and M.thermoautotrophicum ΔH (Fig. 2A; Table 2), while the probe specific for FR-II hybridized with DNA from M.thermoformicicum strains THF, Z-245, FTF, CSM3 and HN4 (Fig. 2B; Table 2).

Table 2. Copy number per chromosome of FR-I and FR-II, respectively, in different strains of the genus *Methanobacterium* 

O'.	Copy numb	ber
Strain	FR-I	FR-II
M.thermoformicicum		
THF	4-5 (pFV1) <sup>1</sup>	5-6 (pFV1 and chromosomal DNA)
Z-245	0	4-5 (pFZ1) <sup>1</sup>
FTF	0	4-5 (pFZ2) <sup>1</sup>
CSM3	3	1
FF1	3	0
FF3	3	0
HN4	0	1
CB12	0	0
SF-4	0	0
M.thermoautotrophicum		
ΔΗ	12	0
Marburg	0	0

<sup>&</sup>lt;sup>1</sup> estimated on the basis of the plasmid copy number (Nölling et al., 1991).

Since three of the hybridizing methanogenic strains were known to contain plasmid DNA, i.e. strains THF, Z-245, and FTF (Nölling et al. 1991), the location of the homologous counterparts of pFV1 was determined. Comparison of the nucleotide sequences of plasmid pFV1 from strain THF and pFZ1 from strain Z-245 (Nölling et al. 1992) had shown that plasmid pFZ1 contained sequences with high similarity to FR-II but not to FR-I (see below). This was confirmed by hybridization with the FR-II probe that showed the expected hybridization pattern of pFZ1 fragments with DNA from strain Z-245 (Fig. 2B, lanes 1 and 4). Since pFZ1 is very similar, if not identical to pFZ2 from strain FTF (Nölling et al. 1991), the latter plasmid should also contain a FR-II-like sequence. Indeed, DNA from both strains Z-245 and FTF showed an identical hybridization pattern (Fig. 2B, lanes 1, 2 and 4, 5).

<sup>&</sup>lt;sup>2</sup> minimal estimation.

These results indicate that *M.thermoformicicum* strains Z-245 and FTF do not harbor chromosomal sequences related to plasmid pFV1. Similarly, no chromosomal copies of FR-I seemed to be present in strain THF since only pFV1-derived restriction fragments showed hybridization with the FR-I probe (Fig. 2A, lanes 3, 6). In contrast, hybridization of *EcoRI*-digested total DNA from strain THF with the FR-II-specific probe revealed, besides the expected pFV1-derived fragment (major hybridization species in Fig. 2B, lane 6), additional hybridizing fragments indicating that strain THF harbors chromosomal sequences with similarity to FR-II. Since strains CSM3 and HN4 lack plasmid DNA (unpublished results), the fragments hybridizing to the FR-II probe are part of the chromosomal DNA of these strains. *M.thermoautotrophicum* Marburg, the other known plasmid-containing *Methanobacterium* strain (Meile et al. 1983), appeared to lack sequences with similarity to plasmid pFV1 (Table 2).

# Characterization of plasmid and chromosomal copies of FR-I

The exact size and location of FR-I was determined by comparison of the nucleotide sequences of pFV1 and pFZ1. FR-I on pFV1, designated FR-Ia, has a size of 1501 bp (ranging from position 2852 to 4352 according to Nölling et al. 1992), contains terminal, 6 bp direct repeats with the palindromic sequence AAATTT and is flanked by sequences of the conserved backbone structure of both plasmids (Fig. 3 and 4). No sequences with similarity to FR-Ia could be identified in pFZ1. However, plasmid pFZ1 contains a 6-bp sequence (AGATTT) at a location (position 3445 to 3450 according to Nölling et al. 1992) that corresponds with that of FR-Ia in pFV1 (Fig. 4). Since this hexamer resembles the terminal AAATTT repeats of FR-Ia, it may represent a target integration site of FR-I which is duplicated upon insertion. The AT-content of FR-Ia (70.3%) and its flanking regions (58%) was clearly dissimilar suggesting that the origin of FR-Ia differs from that of the rest of the plasmids.

The chromosomal counterparts of FR-I were analyzed in *M.thermoautotrophicum*  $\Delta H$  and *M.thermoformicicum* CSM3. Two overlapping fragments of *M.thermoautotrophicum*  $\Delta H$  that hybridized to the FR-I probe, an approximately 4-kb EcoRI (Fig. 2A) and a 1.7-kb ScaI-PstI fragment (data not shown), were isolated from agarose gel and cloned into EcoRI- and SmaI-PstI-digested pUC19, respectively, to yield pU $\Delta H1$  and pU $\Delta H2$  (Table 1; Fig. 3). Both pU $\Delta H1$  and pU $\Delta H2$  share a common 1-kb ScaI-EcoRI fragment.

The nucleotide sequence of a 2766-bp PstI fragment included in pUΔH1 and pUΔH2 was determined (EMBL accession no. X69112) (Fig. 5). Comparison of this sequence with that of FR-Ia from plasmid pFV1 revealed that strain ΔH contains a copy of the FR-I sequence, termed FR-Ib, integrated into a region that shares no similarity with plasmid pFV1. The FR-I elements from strains THF and ΔH showed an identical size but different organization: a 383-bp segment, designated boxII, appeared to be located at either side of a 1118-bp segment, designated boxI (Fig. 3 and 5). The distinct organization of the FR-Ia and FR-Ib elements was confirmed by hybridization experiments using the FR-I-specific probe. As the result of the boxI-boxII organization of FR-Ia (Fig. 3), only a single hybridizing EcoRI fragment, approximately 5.6 kb in size, was generated (Fig. 2A, lane 6). In contrast, since the FR-Ib element displays a reversed organisation of boxI and boxII (Fig. 3), two hybridizing fragments of approximately 4.0 and 1.3 kb were produced upon cleavage with EcoRI (Fig. 2A, lane 8). The sequence of the junction sites of boxI and boxII, AAATTT in pFV1 and ATATTT in strain ΔH, were similar to those found at the ends of FR-I from

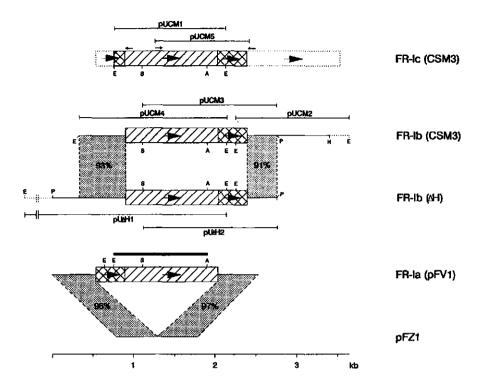


Figure 3. Organization and similarity of different FR-I elements and flanking regions deduced from the nucleotide sequences of the indicated clones described in this study and by Nölling et al. (1993a). Hatched and cross-hatched rectangles in the FR-I elements represent the identical boxI and boxII sequences, respectively. Arrows inside boxI and boxII indicate their orientation. Sequenced regions are denoted by solid lines. FR-Ia represents the FR-I element in plasmid pFV1 from M.thermoformicicum THF, whereas FR-Ib and FR-Ic represent the FR-I elements in the chromosome of M.thermoformicicum CSM3 and M.thermoautotrophicum ΔH, respectively. The presumed extension of FR-Ic is shown by dotted lines. The positions of the FR-I-specific primers used for PCR-amplification of DNA from strain CSM3 are indicated by small arrows. The shaded areas show homologous regions flanking FR-Ib in strains CSM3 and ΔH and those flanking FR-Ia of pFV1 and the corresponding region in pFZ1. The similarity values are indicated in percentages. The restriction fragment of pFV1 used for hybridization as FR-I-specific probe is indicated by a solid bar. Letters denote relevant restriction sites used for the cloning and in hybridization experiments (A, AccI; E, EcoRI; H, HindIII; P, PsI; S, ScaI).

either strain, i.e. each boxI, boxII and the complete FR-I element are flanked by similar terminal direct repeats with the consensus sequence A(A/T)ATTT (Fig. 4). Most remarkably, the nucleotide sequences of boxI and boxII from strains THF and  $\Delta H$  were identical.

M.thermoformicicum CSM3 DNA digested with EcoRI and hybridized with the FR-I probe generated two hybridization signals of approximately 1.4 kb and 2.0 kb with different signal intensity (Fig. 2A, lane 9). To clone those fragments, EcoRI-digested DNA from strain CSM3 ranging in size from 1-3.5 kb was isolated from agarose gel, ligated to pUC19 and introduced in E.coli. Transformants containing DNA that hybridized with the FR-I probe

appeared to harbor one of three plasmids, termed pUCM1, pUCM2 and pUCM3 with inserts of 1.4, 1.3 and 1.8 kb, respectively, (Fig. 3; Table 1). The similar sized inserts cloned in pUCM1 and pUCM2 may explain the differences in signal intensity obtained with the FR-I probe (Fig. 2A). A fourth clone, pUCM4, was constructed by cloning a 1.6-kb ScaI-PstI fragment from strain CSM3 which overlaps with the inserts of pUCM2 and pUCM3, into pUC18 digested with SmaI-PstI (Fig. 3).

Nucleotide sequence analysis of the pUCM3- and pUCM4 inserts and of a 1.2-kb EcoRI-HindIII fragment of the pUCM2 insert yielded a continuous stretch of 3055 bp. Comparison of this sequence to that of FR-I from M.thermoformicicum THF and M.thermoautotrophicum  $\Delta H$  revealed that M.thermoformicicum CSM3 also contains a complete FR-Ib-type element (EMBL accession no. X69113) analogous to the one found in strain  $\Delta H$  (Fig. 3). Direct repeats with the sequence A(A/T)ATTT were flanking either end of boxI, boxII and the entire FR-I element (Fig. 4). Again, the CSM3-derived boxI and boxII were identical on the sequence level with those from strains THF and  $\Delta H$ .

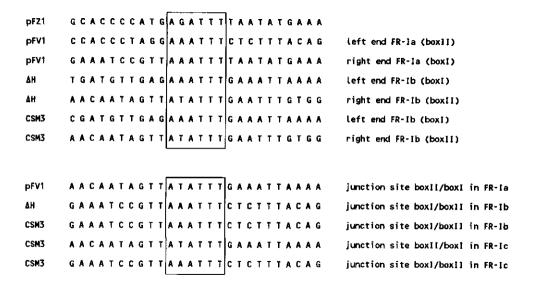


Figure 4. Conserved terminal hexanucleotides in the FR-I elements and boxI-boxII junction sites, respectively. The upper part shows an alignment of the terminal sequences of FR-I elements derived from plasmid pFV1 M. thermoformicicum THF (FR-Ia) and the corresponding region of plasmid pFZ1 from M. thermoformicicum Z-245, and from the chromosome of M. thermoformicicum CSM3 (FR-Ib and FR-Ic) and M. thermoautotrophicum  $\Delta H$  (FR-Ib). The boxI-boxII junction regions of either FR-I element is shown in the lower alignment. The consensus hexanucleotide A(A/T)ATTT is boxed.

Similar to the situation observed in plasmid pFV1 the flanking regions of FR-I in strain CSM3 and  $\Delta H$  also differed in AT-content from that of FR-I, i.e. 45.9% versus 70.3%, respectively. This suggests that these elements have been acquired from another source and integrated into the chromosome. Alignment of an approximately 0.5 kb sequence stretch flanking FR-I from the strains CSM3 and  $\Delta H$  revealed extensive similarity (>90% identity)

PstI CTGCAGGGTGTGACTTCCTGGTATCCGATGACATCCACCCCGCCGACCTGCTGGAGGGGGCACATGGACAGGATACTCAGGAGGGGGGTCGATTACGGTAT 1 101 TGACCCTGTAAGCGCTGTGCAGATGGTCACCATAAACCCTGCGGAGCACTACGGCCTCAGCACAGGGGCAATAGCGCCTGGATGGGATGCTGACTTCGTG 201 GTGGTTGACAGCCTCAGGGACTTCAACGTTAAGAGGGTCTACATAGATGGTAGACCTGTGGCGGATAGGGGCAGATACCTCATCAGGAGATCCGGGGGAA 301  ${\tt CCAGGGCACCCCCAGGAAACTTGAAGTGCCTGATTTTCCAGTTGAGAGATTGAATATCAGGGCTGATGAGGCTGATGAGGCTCATAGATGT}$ 401 ACTGGACGGCCAGCTCATAACTGAAGAGCTAATTGCAACCCTGGAAGTTGAGGACGGCACGGTGCAGGCTGACACGTCCTCAGATATCCTCAGGGTATCT GTCCTTGACAGGTACGGGAGGGGTAATATCTCCAGCGGCTTCGTTCATGGATTCGGCCTCCAGGAGGGGGCAATAGCATCAACAGTTGCCCATGACTCAC 501 BanHl 601 ACAACCTGATCGTGGGGGTGGATCCTGGGCTGATGAAGAGGGCGGTTGATATACTTAAAAAAGCAGGGGGGTCTTGTGCGCGGTCTCAGGGGATGA 701 TCACAGGGTCCTTCAGCTTCCTCTGGCAGGTCTGATGTCAGATGGGGATGTATTTTGAGGTTCCAGATGGATTTGAGAACCTCAACACTTCACTGAACAGC 801 (BoxI). \*\*\*\* <u>GAAATTT</u>GAAATTAAAAACTTAATGGAGATGTGAAAATGGGAGTTAAAGAAGATATTCGTGGACAAATTATAGGAGCATTAGCAGGAGCCGATTTCCCAA 901 Scal TAAATTCACCAGAAGAACTAATGGCAGCGCTTCCAAACGGTCCAGATACTACTTGTAAATCTGGAGATTTAAAAGCATCTGATGCTGGACAAGT 1001 1101 ACTTACTGCTGATGATTTTCCATTTAAAAGTGCTGAAGAAGTTGCAGATACTATAGTGAACAAAGCAGGATTATAAGCCAAAATCGACTTCCTACTTTTT 1201 CTTTCTTTTTTTAAGGATAATTAATTATTATCTTATAATAGGTTTTAATGGAGAAATTAAAATGGATAAGCCCAATAGTAAAGAAAATAAGCATAA 1301 1401  $\textbf{ATAGTTCTGAAACGA} \underline{\textbf{TTA}}\underline{\textbf{TTTTTTCAAATATTTTTTAAAATTACTGAGCA}\underline{\textbf{TTATGAGTAGATTATTCCTFTTTCAGTAATCATATAATCTCCACGTTCA}$ 1501 1601 TGACGCTGCAATATCAAGTCACTTTCAAGTAATTTTTGTATGTGGAAAAGTAAATTACCACCACGACGCCCTGTAAGTTCTGAAAGAGCAGTGAATGTCA 1701 TGGTTTCAGAGGCCATAGATTTAAGAATTTGAAGTCTCTGTTTATTAGAAATAGGTTCAAGAACACTCTTAACCATAATTTCTTCAGGAATAGAAGATAT Acc1 1801 1901 BoxI/BoxII. TATTTTGTAGAAATCCGTTAAATTTCTCTTTACAGGTTTCCCGGATCTTACAGGGGATTAACCATATTTTGTTCTAAATCATTTTCAATATCATCAGAAAT EcoRI ATAAACAGATACTGAATTCAAAATATCCTTTTTTAAGTTGCTTAGCATTAAATCAAGGTATTCTTGATTAGATTTTTCCATCAAACGCTTGATATCCTGA 2101 EcoRI -FR-I(BoxII) GTITCTTTCTTGACCTTTTAGTCATATTTGTGTATAAAACTGTACTTAGTACATTITAATGACGGTTTAGTATATATTTCTAATAAACAATAGTTATATT TTDAATTTGTGGATGTTCTCGTGCCCTGATAGGGGTTAGTTACTTTTCATGGGGCAGCAATCTCATGATATCTTTGATTCAGGGCCTGGATTATCCTCCT 2501 CATGGCCTCCTTCTCCCTGGGGCCCCCGACCTTCCTTGCAACCCGGTTCATCTCAGCGATCCTCTCCCTGAGGACCAGAGGGTCTGAAAATTCAGCTCGC 2601 GTATAGGCTATCAGTGACTCAATAACAGCGTATATGCCACGGTTGAGGGCCATCCTGAAGCTTTCAGCCCTCATAACATCACCTGCACGGGCCTTCACAA Pacl CATGAAGTTCTGACTCACCGAACCGGTCCCTCTTCACCAGCTTCTTCACAGAGACAACCTCTGCAG

Figure 5. Nucleotide sequence of the 2766-bp PstI fragment from  $M.thermoautotrophicum \Delta H$  including FR-Ib and its flanking regions. Boxed nucleotides represent the consensus hexanucleotide located at the ends of FR-I and the junction site of boxI and boxII. The initiation and termination codons of two ORFs (1 and 4) of FR-Ib are marked. Asterisks denote a potential ribosome binding site.

(Fig. 3). Since strains  $\Delta H$  and CSM3 are closely related organisms (Nölling et al. 1993b) this finding suggests that the FR-Ib element is located at identical positions within the same sequence context in the chromosomes of strain  $\Delta H$  and CSM3.

A different result was obtained from sequence analysis of the 1.4-kb EcoRI fragment cloned in pUCM1. It contained the complete boxI of FR-I which seemed to be flanked at both sites by one copy of boxII (Fig. 3). The junction sites of boxI and boxII showed the consensus sequence A(A/T)ATTT (Fig. 4). Since the cloned EcoRI fragment contained only about 100 bp of the adjacent copies of boxII no analysis of the flanking chromosomal sequences was possible. Nevertheless, the sequence of the pUCM1 insert suggests that, in addition to a FR-Ib, strain CSM3 contains another type of FR-I, designated FR-Ic, consisting

of either two copies of boxII and one copy of boxI or representing a tandem repeat of either FR-Ia or FR-Ib (Fig. 3). To discriminate between these possibilities, we analyzed a PCR-amplified DNA fragment that was produced from total DNA of strain CSM3 using two primers specific for boxI of FR-I (see Fig. 3). Sequence analysis of the approximately 1-kb PCR product, which was cloned into *HindII*-linearized pUC19 to yield pUCM5 (Fig. 3; Table 1), revealed that it comprise a complete boxII flanked by sequences homologous to boxI. This result suggests that FR-Ic may consist of at least two continuous copies of either FR-Ia or FR-Ib (Fig. 3).

# Coding capacity of the FR-I elements

The FR-I elements were inspected for the presence of open reading frames (ORFs) with more than 200 bp and appropriate start codons (ATG, GTG or TTG). The boxI of either FR-I element contained an identical ORF, designated ORF1, with a size of 237 bp ranging from position 3264 to 3500 in FR-Ia of strain THF (Nölling et al. 1992) and from position 937 to 1173 in FR-Ib of strain  $\Delta H$  (Fig. 5 and 6). Two additional ORFs were found in FR-Ia of pFV1. One of these, ORF2, was 294 bp in size (ranging from position 3100 to 2809) and part of boxII, while the other one, ORF3, was 258 bp in length (from position 4103 to 3848) and located in boxI (Fig. 6). In FR-Ib of the strains  $\Delta H$  and CSM3, the different organization of boxI and boxII resulted in a fusion of ORF2 and ORF3 yielding ORF4 with a size of 750 bp (ranging from position 2268 to 1519 in strain  $\Delta H$ ; Fig. 5 and 6). However, except for ORF1, none of the ORFs were preceded by a sequence with similarity to a consensus methanogenic ribosome binding site (Brown et al. 1989) (Fig. 5). A TFASTA search (Pearson et al., 1988) of the nucleotide sequence and the deduced amino acid

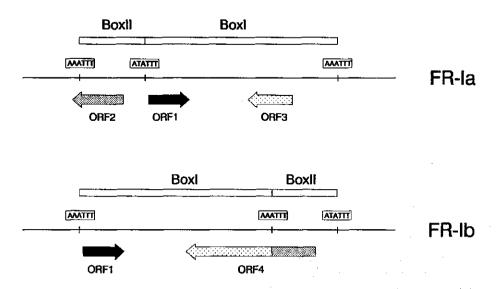


Figure 6. Coding capacity of FR-Ia from plasmid pFV1 of M, thermoformic cum THF and FR-Ib from either M. thermoautotrophicum  $\Delta H$  or M. thermoformic cum CSM3. Identical coding regions are indicated by a similar shading.

sequences of possible gene products of the FR-I elements with those stored in the databases revealed no significant similarity.

# Copy number of FR-I elements

Since the FR-I elements were exclusively plasmid-located in M. thermoformicicum THF, their copy number correspond with that of pFV1 which is present in approximately 4 to 5 copies per chromosome in this strain (Nölling et al. 1991) (Table 2). To determine the copy number of FR-I elements contained in the chromosome of Methanobacterium strains, total DNA of these strains was digested with restriction endonucleases that have no cleavage sites in FR-I, and subsequently hybridized with the FR-I-specific probe. Hybridization of SalI-SphI cleaved DNA prepared from M.thermoformicicum strains CSM3, FF1 and FF3 yielded a single hybridization signal with comparable intensity (Fig. 2A, lanes 13-15). When DNA of the same strains was digested with BamHI and PstI, we observed three hybridization signals with the DNA from strains CSM3 and FF1 and only one with that from strain FF3 (Fig. 2A, lanes 10-12). The obtained hybridization patterns and the signal intensities indicate that strains CSM3, FF1 and FF3 each harbor at least three copies of a FR-I element which are located on BamHI-PstI fragments that differ in size in strains CSM3 and FF1 but are similar sized in strain FF3 (Table 2). Moreover, these multiple FR-I elements seem to be clustered in the strains CSM3, FF1 and FF3 on an approximately 15 kb sized SalI-SphI fragment (Fig. 2A, lanes 13-15).

In the case of *M.thermoautotrophicum*  $\Delta H$ , a single hybridization signal was observed with *Bam*HI-digested DNA (data not shown) and two signals with DNA cleaved by *EcoRI* (FR-I contains two *EcoRI* sites; Fig. 2A, lane 8). These results would indicate that strain  $\Delta H$  contains a single copy of FR-I. However, the comparable signal intensity of the major hybridization species of *EcoRI*-digested  $\Delta H$  DNA (Fig. 2A, lane 8) and that derived from *BamHI-PstI* cleaved FF3 DNA which represents three copies (Fig. 2A, lane 12), suggests that strain  $\Delta H$  may harbor more than one FR-I element (Table 2).

## Characterization of FR-II

Comparison of the nucleotide sequences of plasmid pFV1 and pFZ1 (Nölling et al. 1992) had shown that plasmid pFZ1 contains a region homologous to the 3.3-kb NarI-EcoRI fragment of pFV1 which includes FR-II. Therefore, plasmid pFZ1 also carries a copy of FR-II (designated FR-II'). Due to the high interplasmid similarity of the FR-II containing regions, however, determination of the exact size of FR-II and FR-II' was not possible. To allow for a better comparison, the chromosomal FR-II element of M.thermoformicicum CSM3 was analyzed. For this purpose, we first cloned a 4.5-kb EcoRI fragment of strain CSM3 that hybridized with the FR-II probe (Fig. 2B, lane 9) to yield pUCM6 (Table 1). Sequence analysis of a part of the pUCM6 insert generated a continuous stretch of 2676-bp (EMBL accession no. X69114). Alignment of this sequence with that of the FR-II-containing plasmid regions revealed a 2.5-kb fragment with high similarity. This chromosomal segment of strain CSM3 was designated cFR-II (Fig. 7).

The cFR-II segment comprised 2542 bp (from position 47 to 2568 of the analyzed pUCM6 sequence) and had a similar size as FR-II' from plasmid pFZ1 (2510 bp; position 4750 to 7258 according to Nölling et al. 1992). FR-II from plasmid pFV1 contained, however, a direct repeat of two identical 524-bp sequences (DR) that enlarged its size to 3034 bp

(position 5687 to 8719 according to Nölling et al., 1992).

Both FR-II' and cFR-II contained ORFs of a comparable size, ORF5' (position 5295 to 6791) and cORF5 (position 730 to 2142) (Fig. 7), respectively, that could code for proteins with a calculated molecular mass of respectively 54.1 and 51.6 kDa. Due to the sequence duplication in pFV1, however, two partially identical ORFs, ORF5a (position 6214 to 6221) and ORF5b (position 6890 to 6895), were generated in FR-II that could code for proteins with a calculated molecular mass of 24.7 and 49.6 kDa, respectively (Fig. 7). As a consequence, the C-terminal part of the ORF5a protein and the N-terminal part of the ORF5b protein would share a block of 170 identical amino acids. The plasmid-located ORF5a of pFV1 and ORF5 of pFZ1 are followed by two additional, smaller ORFs, ORF6 (position 8354 to 8719) and ORF6' (position 6831 to 7259), respectively (Fig. 7). The capacity to code for large and highly similar proteins is the most conspicuous feature of the FR-II segments. Alignment of the amino acid sequences deduced from ORF5a/b, ORF5' and cORF5 revealed 72-84% identical residues. Interestingly, cORF5 of strain CSM3 is flanked by sequence blocks which share no homology with the plasmid-located FR-II segments (Fig. 7). This particular conservation of cORF5 and its plasmid-derived counterparts may indicate

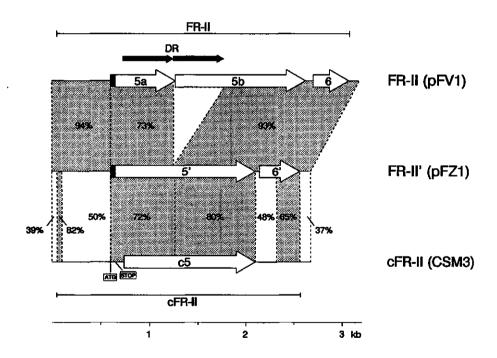


Figure 7. Organization and similarity of the FR-II segments derived from plasmid pFV1 and pFZ1 of *M.thermoformicicum* strains THF and Z-245, respectively, and the chromosome of strain CSM3. ORFs are represented by open arrows whereas the direct repeat (DR) found in pFV1 is indicated by black arrows. The 5'region of ORF5a and ORF5' that could code for a putative signal peptide is indicated by a black block. The position of a stop codon that would result in a N-terminal truncated cORF5 protein of strain CSM3 is shown. Regions with high degree of similarity are shaded and homology values are given in percentages.

their expression into proteins with yet unknown function. A database search failed, however, to detect significant similarities with the nucleotide sequence or the deduced amino acid sequence of either of the FR-II segments.

The ORF5a protein of pFV1 and the ORF5 protein of pFZ1 contained a stretch of 24 amino acids with structural similarities to a prokaryotic signal sequence (Gierasch 1989): a N-terminal located block of four polar and one positively charged residue followed by a hydrophobic core of 13 residues and a putative signal peptidase cleavage site (for ORF5a: NH<sub>2</sub>-MRNGTLVLAALLTLFVLAGSSSA \(\lambda\)DVGIELDKN...; charged and hydrophobic residues are underlined and in italics, respectively; the arrow indicates the putative signal peptidase cleavage site). The presence of this putative leader peptide suggests that the proteins may be translocated through or associated with the cell membrane. The deduced product of cORF5 of strain CSM3, however, lacks this sequence since a stop codon at position 688 would result in a protein which is, compared to the corresponding plasmidencoded proteins. N-terminally truncated by 33 amino acids (Fig. 7).

Inspection for appropriate expression signals suggested that the ORF5a/ORF5b region of plasmid pFV1 may form a transcriptional unit since a sequence stretch with considerable similarity to a typical archaeal promoter signal (Hain et al. 1991) could be identified upstream ORF5a, whereas ORF5b is immediately followed by a T-rich stretch that resembled a conserved archaeal transcription termination signal (Brown et al. 1989). Both ORFs are preceded by a potential ribosome binding site (Brown et al. 1989). The putative transcription and translation signals identified for ORF5' of pFZ1 were almost identical to those found for ORF5a/ORF5b, i.e. ORF5' displays the promoter sequence and the ribosome binding site of ORF5a and the terminator signal of ORF5b. Similar transcription signals could be identified for the chromosomal cORF5 although it is devoid of a appropriate ribosome binding site.

## DISCUSSION

The high similarity of the archaeal plasmids pFV1, pFZ1 and pFZ2 from *M.thermoformicicum* strains THF, Z-245 and FTF, respectively, suggested by hybridization studies (Nölling et al. 1991) and partially confirmed by nucleotide sequence analysis (Nölling et al., 1992), implies that these extrachromosomal elements belong to a family of related plasmids and probably have been derived from a common ancestor. Whereas the major part of the plasmids consist of unique sequences which showed no homology to chromosomal DNA of the methanogenic strains used in this study, two regions of plasmid pFV1 could be identified that have chromosome-located counterparts in several thermophilic strains of the genus *Methanobacterium*. One of those plasmid-derived regions, FR-I, is characteristic for plasmid pFV1, whereas the other one, FR-II, is also part of plasmids pFZ1 and pFZ2.

FR-I consists of two sequence blocks, boxI and boxII, which occur in a variable sequential order. Based on their organization three different types of FR-I could be identified (Fig. 3): (i) FR-Ia, which is part of plasmid pFV1, displays a boxII-boxI organization; (ii) FR-Ib, isolated from the chromosome of *M.thermoautotrophicum*  $\Delta H$  and *M.thermoformicicum* CSM3, with the order boxI-boxII; and (iii) FR-Ic from strain CSM3 consisting of tandemly repeated copies of either FR-Ia or FR-Ib. In spite of their different organization, boxI and boxII of each element have the same orientation (Fig. 3) and an identical nucleotide sequence. FR-Ia and FR-Ib are 1501 bp in size and exhibit defined short terminal direct repeats with the consensus sequence A(A/T)ATTT. Moreover, this consensus sequence

defines the boundaries of boxI and boxII (Fig. 4). The observed different organization of boxI and boxII could well be the result of recombination. It may be suggested that either the A(A/T)ATTT sequence is involved in the rearrangement of boxI and boxII or, alternatively, that the elements containing only a single boxI, i.e. FR-Ia and FR-Ib, represent deletion derivatives of a FR-Ic-like element. The single FR-Ib element found in strain CSM3, for instance, could have been generated from a FR-Ic-type element consisting of two repeated FR-Ib copies by homologous recombination between those repeated elements.

An exceptional property of the FR-I elements is their complete conservation on the sequence level as found for four independently isolated copies from three different *Methanobacterium* strains. A similar observation was reported for the halobacterial insertion sequences ISH1 (Simsek et al. 1982; Pfeifer and Ghahraman 1991) and ISH2 (DasSarma et al. 1983; Pfeifer and Ghahraman 1991). Analogous to the 520-bp ISH2 element, also the FR-I elements have low coding capacity, indicating that other characteristics than the encoded gene products might be responsible for the conservation on the nucleotide level. One may argue that the examined strains have recently acquired these elements, and therefore base variations are unlikely to have occurred during this timespan. However, all methanogenic strains that contain at least one copy of an FR-I type were isolated from geographically very different locations during a period of two decades.

It is tempting to speculate that FR-I represents a new archaeal insertion element. Several observations would support this hypothesis. (i) The FR-I elements exist in multiple genomic copies. At least two of the elements, FR-Ia and FR-Ib, are part of a different sequence context as revealed from sequence comparison of the FR-I flanking regions. Since the flanking regions showed no sequence similarity to the FR-I elements, integration of the elements is unlikely to have occurred by homologous recombination. (ii) Each FR-I element contains terminal direct repeats with the consensus sequence A(A/T)ATTT. This direct repeat may either be part of the element or may represent a target site duplication generated upon integration of FR-I. The latter possibility would be supported by the fact that plasmid pFZ1 from strain Z-245 contains a single copy of a similar hexanucleotide, AGATTT, at the position where FR-I is integrated in plasmid pFV1 (Fig. 5). (iii) The FR-I elements contain ORFs that may encode proteins involved in movement of the elements. Since, however, rearrangements of boxI and boxII affect the coding capacity, the major 750-bp ORF is only found in FR-Ib and FR-Ic (Fig. 6).

In contrast to most of the IS elements known in Archaea and Bacteria, FR-I lacks terminal inverted repeats. However, transposition does not depend on the presence of terminal inverted repeats as was found for several transposons from gram-positive bacteria, such as Tn554 (Murphy and Löfdahl 1984) or Tn5276 (Rauch and de Vos 1992). Similarly, no terminal inverted repeats were found for the (putative) insertion element ISH1.8 associated with phage  $\Phi H$  of the archaeon Halobacterium salinarium (Schnabel et al. 1984). The latter authors concluded that the insertion mechanism of those elements is different from that of IS elements with terminal inverted repeats. This could also apply to FR-I. The conclusion, however, that FR-I is a novel type of IS element will only be justified by the observation of its transposition.

A second region of plasmid pFV1, FR-II, was found to have homologous counterparts in the chromosome of *M.thermoformicicum* strains CSM3 and HN4. Furthermore, a chromosomal copy of FR-II seems also to be present in strain THF, the host of plasmid pFV1. In contrast to FR-I, FR-II is an integral part of plasmid pFV1 and pFZ1 and possibly also of the postulated common ancestor of those related plasmids. The presence of FR-II in a restricted number of strains on either plasmid or chromosomal DNA suggests that it belongs

to a similar class of elements as FR-I. However, compared to FR-I, FR-II differs in several aspects: (i) FR-II is also part of the plasmids pFZ1 and pFZ2 of the strains Z-245 and FTF, respectively; (ii) it is less frequently distributed among other thermophilic *Methanobacterium* strains (Table 2); (iii) only a single copy of FR-II seems to be located on chromosomal DNA (Table 2); (iv) FR-II is less conserved on the nucleotide level; (v) there is no evidence for target site duplication; (vi) it displays a higher coding capacity. The most remarkable characteristic shared by the analyzed two plasmid-located FR-II segments and the chromosomal one from strain CSM3 is the presence of a large coding region that may direct the synthesis of highly similar proteins. The high conservation of the FR-II coding regions may indicate that they encode proteins with yet unknown function.

The distribution of FR-I among thermophilic Methanobacterium strains strongly correlates with their phylogenetic position. As was shown by DNA-DNA hybridization studies and 16S rRNA analysis, all FR-I carrying strains, i.e. M.thermoformicicum strains THF, CSM3, FF1 and FF3, and M.thermoautotrophicum  $\Delta$ H, belong to the same species (Touzel et al. 1991; Nölling et al. 1993). We can imagine two explanations for this finding. Either FR-I was already part of the common ancestor of those strains or its dissemination is the result of horizontal gene transfer. The fact that the strains have been isolated from geographically very different locations, would argue for the first possibility. If so, this would imply that the strains Z-245 and FTF, which belong to the same species as the FR-I harboring strains (Touzel et al. 1992; Nölling et al. 1993) but lack FR-I, have lost this element. On the other hand, lateral gene transfer of FR-I may have occurred analogous to dissemination of insertion elements in Bacteria via plasmids or phages. In this case plasmid pFV1 from strain THF may have served as vector in mobilizing FR-I from one strain to another.

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Characterization of the archaeal, plasmid-encoded type II restriction-modification system *Mth*TI from *Methanobacterium thermoformicicum* THF: homology to the bacterial *Ngo*PII system from *Neisseria gonorrhoeae* 

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# Characterization of the Archaeal, Plasmid-Encoded Type II Restriction-Modification System MthTI from Methanobacterium thermoformicicum THF: Homology to the Bacterial NgoPII System from Neisseria gonorrhoeae

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A restriction-modification system, designated MthTI, was localized on plasmid pFV1 from the thermophilic archaeon Methanobacterium thermoformicicum THF. The MthTI system is a new member of the family of GGCC-recognizing restriction-modification systems. Functional expression of the archaeal MthTI genes was obtained in Escherichia coli. The mthTIR and mthTIM genes are 843 and 990 bp in size and code for proteins of 281 (32,102 Ba) and 330 (37,360 Ba) amino acids, respectively. The deduced amino acid sequence of M.MthTI showed high similarity with that of the isospecific methyltransferases M.NgoPII and M.HaeIII. In addition, extensive sequence similarity on the amino acid level was observed for the endonucleases R.MthTI and R.NgoPII. Moreover, the endonuclease and methyltransferase genes of the thermophilic MthTI system and those of the Neisseria gonorrhoeae NgoPII system show identical organizations and high (54.5%) nucleotide identity. This finding suggests horizontal transfer of restriction-modification systems between members of the domains Bacteria and Archaea.

Type II restriction-modification (R/M) systems are composed of two enzymatic activities, an endodeoxyribonuclease (ENase) and a DNA methyltransferase (MTase), which recognize the same specific DNA sequence (44). It has been proposed that a major function of R/M systems is the protection of resident DNA against contamination by sequences of foreign origin (16). A great variety of R/M systems have been identified in prokaryotes (13, 30) and appeared to be valuable tools for studying evolution at the gene and protein levels (44).

Genetic characterization of R/M systems showed that the ENase and MTase genes are usually located in close proximity to each other, although their relative orientations may differ (44). Comparison of ENases and MTases from sequenced R/M systems revealed that ENases share no protein similarity with isospecific MTases. In addition, ENases generally show no homology with other ENases (18), with the exception of the pairs R. EcoRI-R. RsrI (36) and R. BsuFI-R.MspI (12). In contrast, considerable similarities between various MTases were found at the amino acid level, especially between those generating 5-methylcytosine (m<sup>5</sup>C-MTases) (15, 19, 26, 37). Among R/M systems with m<sup>5</sup>C-MTases, those that recognize the target sequence GGCC are widely distributed (30). Representatives that have been sequenced include HaeIII (35), NgoPII (37, 38), BsuRI (14), and BspRI (27). In addition, the sequences from three GGCC-specific MTases from Bacillus subtilis phages SPR, φ3T, and ρ11, have been determined (1, 41). This molecular characterization of GGCC-specific R/M systems allowed the identification of conserved sequence motifs such as the target-recognizing domains in the MTases and the study of the evolution of these proteins (1, 17-19, 43).

All known sequenced R/M systems originate from members of the domain Bacteria; no sequences of ENases or

MTases have been reported from members of the domain Archaea, a fundamentally different group of prokaryotes with a unique phylogenetic position (46). Nevertheless, R/M systems have been detected in representatives of all archaeal groups, including halobacteria (25), thermoacidophiles (28), and several methanogens (20, 33, 39).

In this communication, we describe the characterization of a GGCC-recognizing R/M system, designated MthTI, from the thermophilic archaeon Methanobacterium thermoformicicum THF. This R/M system was initially detected during molecular characterization of a new plasmid, pFVI, that was recently identified in this strain (23). Unexpectedly, the gene and deduced amino acid sequences of the MthTI system showed significant sequence identity with those of the NgoPII system of Neisseria gonorrhoeae, suggesting horizontal gene transfer between members of the Archaea and Bacteria.

#### MATERIALS AND METHODS

Bacterial strains and plasmids. M. thermoformicicum THF (DSM 3848) was cultivated as described previously (23). Escherichia coli JM83 (47) and TG1 (9) were used for subcloning and propagation of plasmids pUC18 and pUC19 (47) and phages M13mp18 and M13mp19 (47), respectively. Expression of the mthTIR and mthTIM genes was analyzed in E. coli HB101 (2). E. coli strains were grown at 37°C in L broth, if appropriate in the presence of ampicillin (50 µg/ml), and handled according to established procedures (31).

The entire 13.5-kb plasmid pFV1 from M. thermoformicicum THF (24) was cloned into a \( \lambda \) GEM-12 vector (Promega Biotec, Madison, Wis.) by using the single XhoI site of pFV1, yielding phage \( \lambda \) GFV1 (24). For construction of plasmids pUV1 and pUV2, two XhoI-SstI fragments, 7.4 and 6.1 kb in size, of \( \lambda \) GFV1 were subcloned into pUC19 digested with SalI and SstI. Plasmid pUV1 was used as a substrate in endonuclease and methylase assays. Plasmid

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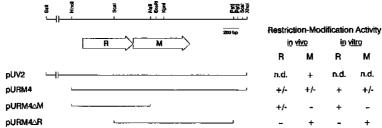


FIG. 1. Restriction map and subclones of a 6.1-kb Sstl-Xhol fragment of plasmid pFV1 containing the MthTl system. Arrows indicate the orientation of the ENase (R) and MTase (M) genes. The in vivo and in vitro ENase (R) and MTase (M) activities of the subclones are summarized. +/-, partial activity; n.d., not determined.

pUV2 carries the MthTI R/M system (Fig. 1). For expression studies in E. coli, a 2.9-kb HindII-HindIII fragment from plasmid pUV2 was cloned into pUC18 digested with HindII and HindIII, yielding plasmid pURM4 (Fig. 1). Deletion of a 1.6-kb fragment between the PstI site of the polylinker and the NsiI site of the insert of plasmid pURM4 resulted in plasmid pURM4ΔM (Fig. 1). For construction of plasmid pURM4ΔR (Fig. 1), a 1.95-kb Scal-PstI fragment from plasmid pUV2 was cloned into pUC18 digested with SmaI and PstI.

Enzymes and chemicals. Restriction enzymes, T4 DNA ligase, and Klenow DNA polymerase were obtained from Life Technologies Inc. (Gaithersburg, Md.). M.HaeIII was purchased from New England Biolabs, Inc., Beverly, Mass. Oligonucleotides were synthesized with a Biosearch Cyclone DNA synthesizer (New Brunswick Scientific Corp.) at The Netherlands Institute for Dairy Research. [α-<sup>32</sup>P]dATP (110 TBq/mmol) was purchased from Amersham International (Amersham, United Kingdom).

DNA manipulations and sequence analysis. Isolation of plasmids, transformation of E. coli, restriction mapping, agarose gel electrophoresis, and subcloning of DNA fragments were done essentially as described previously (31). For determination of the nucleotide sequence, DNA fragments from plasmid pUV2 were isolated from agarose gel, using a Geneclean kit as described by the supplier (Bio 101, La Jolla, Calif.), and subcloned into M13mp18/19 vectors. The nucleotide sequences of overlapping fragments of both strands were determined with use of vector- and insertspecific primers by the dideoxy-chain termination method (32) with the Sequenase kit according to the recommendations of the manufacturer (United States Biochemical Corp., Cleveland, Ohio). Computer analysis of sequence data was done with the University of Wisconsin Genetics Computer Group package (version 6.0) (7) and the CAOS/CAMM facilities at Nijmegen, The Netherlands.

Preparation of cell extracts. Ten-milliliter overnight cultures of E. coli HB101 carrying (part of) the MthTI R/M system were diluted with 10 ml of medium and induced with 2 mM isopropylthiogalactopyranoside (IPTG). After 4 h of growth, cells were harvested by centrifugation and washed in prechilled lysis buffer (100 mM NaCl, 10 mM EDTA, 10 mM β-mercaptoethanol, 50 mM Tris-HCl [pH 7.6]). Finally, cells were resuspended in 0.05 volume of lysis buffer and disrupted by sonication. After heat treatment for 10 min at 65°C (34), the extract was centrifuged for 2 min at 15,000 × g. The supernatant was collected, adjusted to 0.4 µg of protein per µl, mixed with 1 volume of glycerol, and stored at -20°C.

For preparation of cell extracts from M. thermoformicicum THF, approximately 0.1 g of cells was resuspended in 0.5 ml of lysis buffer and disrupted by sonication as described above. After centrifugation, the supernatant, which contained about 3.5 to 5.0  $\mu g$  of protein per  $\mu l$ , was collected, mixed with 1 volume of glycerol, and stored at  $-20^{\circ}\mathrm{C}$ .

Endonuclease assay. Standard assays with R.MthTI were performed in a total volume of 10  $\mu$ l containing 1  $\mu$ g of DNA, 1  $\mu$ l of restriction endonuclease buffer (1 M NaCl, 0.1 M MgCl<sub>2</sub>, 0.01 M dithioerythreitol, 0.5 M Tris-HCl [pH 7.6]), and 1  $\mu$ l of cell extract. After incubation for 1 h at 65°C, the resulting DNA fragments were analyzed by agarose gel electrophoresis.

Methylase assay. For methylase assays with M.MthTI, 1 μl of cell extract was incubated with 1 μg of DNA in 50 mM NaCl-1 mM dithiothreitol-50 mM Tris-HCl (pH 8.5)-0.08 mM S-adenosylmethionine (AdoMet) in a total volume of 5 μl. After incubation for 1 h at 65°C, 12 μl of deionized H<sub>2</sub>O, 2 μl of restriction endonuclease buffer, and 1 μl of extract prepared from E. coli(pURM4ΔM) or 10 U of R.HaeIII were added, and the mixture was incubated for another hour at 65 or 37°C, respectively. Subsequently, the DNA was analyzed by agarose gel electrophoresis. Assays using M.HaeIII were performed under similar conditions but at 37°C.

Primer extension. Approximately 1 µg of pUV1 DNA was incubated under endonuclease conditions with extract prepared from E. coli harboring plasmid pURM4DM or R. Hae III. Digestion of the DNA was checked by agarose gel electrophoresis. The DNA was deproteinized by a repeated double phenol-chloroform extraction and chloroform extraction, precipitated with ethanol, and finally resuspended in deionized H2O. After alkali denaturation, the DNA was precipitated again and resuspended in 5  $\mu$ l of deionized  $H_2O$ . Addition of 2 µl of buffer (0.1 M Tris-HCl [pH 8.0], 0.05 M MgCl<sub>2</sub>) and 3 µl of primer (0.5 pmol/µl) was followed by annealing for 15 min at 37°C. The suspension was mixed with 1 μl of 0.1 M dithiothreitol, 2 μl of deoxynucleoside triphosphate (dNTP) solution (dCTP, dGTP, and dTTP; 1.5 µM each), 0.2 μl of [α-32P]dATP (10 μCi/μl), and 5 U of Klenow DNA polymerase and incubated for 5 min at room temperature. After addition of 4 µl of chase solution (all four dNTPs; 0.5 mM each), the mixture was incubated for 30 min at room temperature; the reaction was stopped by addition of 8 µl of the stop solution used for the sequence reactions.

Nucleotide sequence accession number. The nucleotide sequence reported in this paper has been assigned the GenBank accession number M97222.

### RESULTS

Identification and sequence analysis of the MthTI R/M system. The thermophilic M. thermoformicicum strain THF harbors the 13.5-kb plasmid pFV1 (24). During restriction analysis of pFV1, we observed that its DNA was resistant to digestion with the GGCC-specific ENase R. HaeIII. Upon cloning of the two XhoI-SstI fragments of pFV1 in E. coli JM83 by using pUC19, it appeared that DNA of one of the resulting plasmids, pUV1, was sensitive to R. HaeIII. In contrast, DNA of the other plasmid, pUV2 (Fig. 1), was only partially digested with R.HaeIII despite the presence of multiple HaeIII recognition sites in at least the vector part of pUV2. The degree of protection against digestion with R.HaeIII increased when the mcrB E. coli strain HB101 was used to propagate pUV2 (Fig. 1). These results indicate that M. thermoformicicum THF contains an MTase activity, designated M.MthTI, which modifies the R.HaeIII recognition sequence and is probably encoded by the insert DNA of pUV2. Subcloning of pUV2 DNA followed by R. Hae III digestion studies allowed the location of the putative mthTIM gene on a 1.95-kb ScaI-PstI fragment, contained in plasmids pURM4 and pURM4 DR. These plasmids were partially and completely resistant to digestion by R. HaeIII, respectively (Fig. 1; see below).

Nucleotide sequence analysis of the 2,879-bp HindII-XhoI insert present in pURM4 (Fig. 2) revealed two large, partially overlapping open reading frames (ORFs). The first ORF is located between positions 166 and 1032. This ORF contains an initiation codon (ATG) at position 187, which is preceded by a potential ribosome binding site (positions 171 to 181). If this initiation signal is used, the ORF could code for a protein with 281 amino acids (32,102 Da). Since plasmids containing this ORF resulted in an ENase activity in *E. coli* (Fig. 1; see below), we conclude that it represents the mthTIR gene. The second ORF ranges from positions 1026 to 2019 and is included in the 1.95-kb Scal-PstI fragment, which specifies MTase activity (see below). Therefore, we conclude that this ORF contains the mthTIM gene. A potential start site of the mthTIM gene is the second triplet of this ORF (ATG at position 1029), which partially overlaps with the opal stop codon (TGA) of the preceding mthTIR gene. The mthTIM gene is preceded by a putative ribosome binding site at positions 1014 to 1018. If this ATG is used, the mthTIM gene could code for a protein of 330 amino acids (37,360 Da).

Preceding the coding regions of each gene, two possible transcription initiation sites with similarities to a typical methanogenic promoter (4, 29) consisting of a consensus boxA and a boxB could be identified (Fig. 2), but their functionality has to be verified. Immediately following the mthTIR gene, a T stretch that could function as a transcription termination signal was observed (Fig. 2) (4). A second T-rich stretch was identified downstream of the translation termination codon of mthTIM. This putative transcription termination signal is contained within a 198-bp region consisting of several direct repeats (Fig. 2), which were not found elsewhere in the DNA of pFV1 (24).

Activity and recognition sequence of R.MthTI. Plasmids pURM4 and pURM4ΔM, which both contain the mthTIR gene under control of the vector-located lac promoter (Fig. I), appeared to encode active ENase, since E. coli HB101 harboring either of those plasmids showed low recovery and substantial degradation of plasmid DNA (data not shown). To analyze the in vitro ENase activity, cell extracts prepared from E. coli HB101 harboring pURM4ΔM were incubated

with phage λ and pUV1 DNA at 65°C. The results showed that the number and size of the restriction fragments obtained with the extract were identical to those obtained by digestion with purified R.HaeIII at 37°C (Fig. 3A). Similar digestion patterns were obtained with cell extracts prepared from cells, of HB101 harboring pURM4 (Fig. 1) and M. thermoformicicum THF, although the activity of the latter extracts was much lower than that of the E. coli extracts. No ENase activity was found in control experiments using clones with either pURM4ΔR or pUC18 (data not shown). These results confirm that the M. thermoformicicum R.MthTI activity is encoded by the cloned, pFV1-located mthTIR gene. In addition, the data indicate that the archaeal R.MthTI recognizes the same DNA target sequence as does R.HaeIII, i.e., GGCC (3).

To determine the exact position at which R.MthTl cleaves the target sequence, primer extension experiments were performed, using R.MthTl- or R.HaeIII-digested pUV1 DNA as a template. The primer extension product of DNA incubated with R.MthTl was the same size as that derived from incubation with R.HaeIII (Fig. 4). Inspection of the sequence ladder run in parallel showed that both ENases cleave the target sequence to yield  $GG \downarrow CC$ .

Activity of M.MthTI in vivo and in vitro. To extend the observation that pUV2 DNA and DNA of some of its subclones (Fig. 1), when propagated in E. coli HB101, showed (partial) resistance to digestion with R. Hae III, those plasmids and control DNAs were incubated with R.MthTI obtained from a cell extract of E. coli HB101 harboring pURM4ΔM. As was expected from the identical target site recognition of the two ENases, the same protection against digestion was observed. Remarkably, DNA of pUV2 and pURM4 was only partially protected against digestion by both R.HaeIII and R.MthTI, whereas DNA of pURM4ΔR was found to be fully protected against digestion by both ENases (not shown), suggesting different expression levels of the mthTIM gene in E. coli harboring these plasmids. Low M.MthTI activity was also observed in extracts of E. coli HB101 harboring pURM4, which contains the complete MthTI R/M system under control of the vector-located lac promoter (Fig. 1). Higher MTase activity was observed in cells containing pURM4AR, and almost complete protection of pUV1 DNA against restriction with either R. HaeIII or pURM4ΔM-encoded R.MthTI was found (Fig. 3B, lanes 1 to

In vitro methylation assays using a cell extract of E. coli HBI01(pURM4AR) clearly showed the dependence of the M.MthTI activity on addition of the methyl group donor AdoMet (Fig. 3B, lanes 1 to 4). Similar dependence on AdoMet was obtained when pUV1 DNA was modified in vitro with M.HaeIII at 37°C (Fig. 3, lanes 5 to 8). Furthermore, extracts from M. thermoformicicum THF also contained AdoMet-dependent MTase activity which gave protection against R.HaeIII or R.MthTI (not shown). However, this in vitro activity was lower than that observed in E. coli extracts harboring pURM4AR. These results demonstrate that the mthTIR and mthTIM genes are both components of the GGCC-recognizing R/M system MthTI.

M.HaeIII modifies the tetranucleotide target sequence at the third position, yielding GG<sup>me</sup>CC (22). Since DNA modified by M.MthTI is resistant to digestion with R.HaeIII (Fig. 3B, lanes 2 and 4) and, vice versa, DNA modified by M.HaeIII is also resistant to digestion of the pURM4ΔM-encoded R.MthTI (Fig. 3B, lanes 5 and 7), it is likely that M.MthTI modifies the target sequence at the same position as that modified by M.HaeIII.

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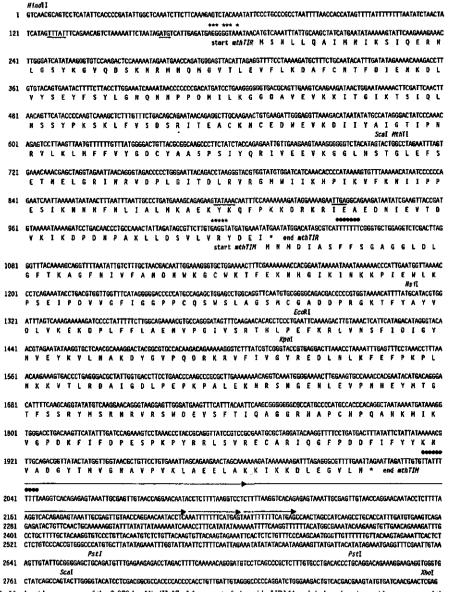


FIG. 2. Nucleotide sequence of the 2,879-bp *Hindl1-Xho1* fragment of plasmid pURM4 and deduced amino acid sequences of the *mthTIR* and *mthTIM* genes. The potential ribosome binding sites are marked by asterisks. Putative archaeal promoters and terminator structures (4, 29) are indicated by lines and circles, respectively. Arrows denote the location of direct repeats downstream from *mthTIM*.

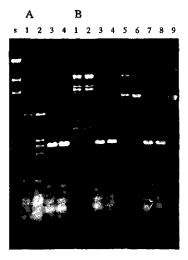


FIG. 3. In vitro ENase (A) and MTase (B) assays of extracts of E. coli HBI01 containing cloned mthTIR and mthTIM genes and purified R. HaeIII and M. HaeIII. (A) Lanes: 1 and 3, DNA of phage  $\lambda$  and plasmid pUV1, respectively, incubated with extract prepared from E. coli harboring pURM4AM; 2 and 4, same DNA as in lanes 1 and 3 but incubated with R. HaeIII (10 U). (B) Lanes: 1 to 4, plasmid pUV1 DNA incubated under MTase assay conditions with an extract prepared from E. coli harboring pURM4AR with (lanes 1 and 2) and without (lanes 3 and 4) AdoMet and reincubated under ENase assay conditions with extract prepared from E. coli harboring pURM4AM (lanes 1 and 3) and 10 U of R. HaeIII (lanes 2 and 4); 5 to 8, same as lanes 1 to 4 except that M. HaeIII (2.5 U) was used in the MTase assay; 9, undigested plasmid DNA from pUV1 (1 μg). Lane s, size marker phage  $\lambda$  DNA (0.5 μg) digested with HindIII.

Sequence comparison of R.MthTI. The nucleotide and deduced amino acid sequences of the R.MthTI enzyme were compared with published sequences of other GGCC-recognizing endonucleases R.NgoPII (38) and R.BsuRI (14). Interestingly, extensive sequence identity was found between R.MthTI and R.NgoPII (Fig. 5), and less, but still significant, identity was found between short stretches of amino acids of R.MthTI and R.BsuRI (data not shown). The high degree of identity (Fig. 5) between R.MthTI and R.NgoPII on the amino acid level (44.8% identity and 67.8% similarity).



FIG. 4. Primer extension analysis of pUV1 DNA digested with R.HaeIII (lane 1) or R.MthTI (lane 2). The primer used had the sequence 5'-CTGTAGTTCAGGATC (positions 377 to 363 of plasmid pFV1) (24). Arrows indicate the extension product and its main 5' nucleotide derived from incubation with both ENases. A shorter extension product attributed to nonspecific termination is also present. A DNA sequence ladder run in parallel is shown at the right.

### M. THERMOFORMICICUM MthTI R/M SYSTEM

R. <u>Meh</u> TI R. <u>Mgo</u> PII	MSNLLQAINVIKSIQERNLGSYKGVQDSRHRHNQHGVTLEVFLKDAFONT 	50 46
R. <u>Mth</u> TI R. <u>Mgo</u> PlI	FDIEMKDLV. YSRYFSYLGNONNPPDMILKGGDAVEVKRITGIKTSIQL 	98 96
R. <u>Mth</u> TI R. <u>Mgo</u> PII	HSSTPKSKLFVSDSRITEACKNCEDWEVKDIITAIGTIPHRV.LKLHFFV	14
R. <u>Mth</u> TI R. <u>Ngo</u> PII	YGDCYAASPSIYQRIVKEVKGGL.BSTGLEPSETMELGRINRVOPLGITD  }	19
R. <u>Mth</u> TI R. <u>Ngo</u> PII	LRYRCHMIIKHPIKVEKMIIPPESIKNNEHLIALMKAKKYRQPPKKDRK	24 24
R. <u>Mth</u> TI R. <u>Mgo</u> PII	R1EAEDHIEVTDVRIKDPDNPARLLDSVLVRYDEI : : : :::::::::::::::::::::::::::::::	28

FIG. 5. Amino acid sequence alignment of R.MthT1 and R.NgoPII. Lines denote identical amino acid residues, colons indicate conservative replacements, and single dots represent gaps. The alignment is based on the program BESTFIT of the University of Wisconsin Genetics Computer Group software (7). Regions with high amino acid identity are underlined.

and on the DNA level (53.3% identity) indicates a close relationship between the two enzymes, which is also reflected in their similar sizes (about 32 kDa each). Several highly conserved regions, comprising 13 to 34 amino acids each with 69 to 76% identity, could be identified (Fig. 5). Except for a conserved region located at the C terminus, both enzymes were most conserved in the central part.

Amino acid sequence comparison of M.MthTI. Following alignments of amino acid sequences of several m5C-MTases, a common architecture of these enzymes was postulated and 10 conserved blocks of amino acid residues were identified (19, 26). Those conserved domains are present with the same sequential order in the M.MthTI protein sequence (Fig. 6). In addition, the variable region between boxes VIII and IX, which is believed to be responsible for sequence specificity (19), shared high similarity with the corresponding region found in the four characterized monospecific GGCCrecognizing MTases (M.HaeIII, M.NgoPII, M.BsuRI, and M.BspRI). These four MTases can be subdivided by size: M.HaeIII and M.NgoPII (37.7 and 38.5 kDa, respectively) and M.BsuRI and M.BspRI (49.6 and 48.3 kDa, respectively). M.MthTI (37.4 kDa) showed the highest degree of amino acid similarity (69.2 and 68.3%, respectively) with M.HaeIII and M.NgoPII (53 and 51.9% identity, respectively; for comparison with M.NgoPII, its alternative start site 12 amino acids downstream of the first Met was chosen). These high similarities are also reflected on the nucleotide level of the corresponding genes (55.3 and 55.9% identity, respectively). Comparison of M.MthTI with M.BsuRI and M.BspRI revealed 47.7 and 43.4% amino acid identity, respectively. This extensive sequence identity and the similar sizes of the enzymes suggest a common ancestor for the mthTIM, haeIIIM, and ngoPIIM genes.

Although the overall similarity between the MTases with GGCC specificity is very high, several residues within the conserved regions showed variations in the M.MthTI enzyme. The most prominent one is a Pro residue at position 52

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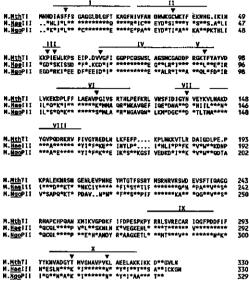


FIG. 6. Amino acid sequence alignment of M.MthTl, M.HaeIII, and M.NgoPII, determined by using the program BESTFIT of the University of Wisconsin Genetics Computer Group software (7). The 11 putative N-terminal amino acid residues of the M.NgoPII sequence have been omitted. The amino acids identical to those of M.MthTl in sequences of M.HaeIII and M.NgoPII are indicated by asterisks. Single dots denote gaps. Regions marked I to X are conserved blocks found in the amino acid sequence of m<sup>5</sup>C-MTases according to Posfai and coworkers (26). Positions marked with arrowheads represent unique amino acid substitutions in M.MthTl compared with m<sup>5</sup>C-MTases and 5'-GGCC-recognizing MTases.

(box III) of the M.MthTI sequence, which is invariably an Asp in all m\*C-MTases analyzed to date (19, 26, 47). Similarly, other single amino acid substitutions at invariant positions of GGCC-recognizing MTases affect the local charge, e.g., replacement of the positively charged Arg residues by Pro and Thr residues at positions 114 (box VI) and 303 (box X), respectively, of the M.MthTI enzyme. In general, there is a tendency toward more hydrophobic substitutions in the conserved regions in the M.MthTI protein, although the overall hydrophobicity of M.MthTI is similar to that of M.NgoPII and M.HaeIII.

### DISCUSSION

In this report, we describe the identification and characterization of the GGCC-recognizing R/M system MthTl from M. themoformicicum THF, which to the best of our knowledge is the first published archaeal R/M system analyzed at the nucleotide level. Characterization of the MthTl R/M system revealed new features with respect to its genomic location, similarity to other R/M systems, and thermostability. The mthTlR and mthTlM genes appeared to be located on the 13.5-kb plasmid pFV1 isolated from M. thermoformicicum THF (23). All plasmids isolated so far from methanogenic bacteria are cryptic (4). Therefore, pFV1 is the first

plasmid in methanogens that codes for identified enzymatic activities.

It was previously reported that the ngoPIIM gene could be cloned only in an mcrB E. coli host (37). This limitation was attributed to the fact that the ngoPIIM gene encoded an MTase that generates methylated DNA with the sequence GGmeCC which is a substrate for the mcrB endonuclease. Nevertheless, we could easily clone the MthTI system in E. coli JM83, which is described as mcrB proficient (47). Since we observed that plasmids carrying the mthTIM gene were only partially resistant to R. HaeIII when propagated in E. coli JM83, limited expression of the mthTIM gene could be a simple explanation for the viability of this host. Alternatively, it could be argued that M.MthTI did not modify the target sequence to yield GG<sup>me</sup>CC but that either GGC<sup>me</sup>C or GG<sup>hme</sup>C<sup>hme</sup>C is hydroxymethylcytosine) was produced. However, these options are not very likely because R.HaeIII is capable of cutting GGCmeC (22) and DNA modified by M.MthTI was resistant to cleavage by R.HaeIII. In addition, hydroxymethylation of cytosine has not been described for type II MTases.

Plasmid pURM4\(\Delta\mathbb{M}\), which contains only the mthTIR gene, could be maintained in a modification-deficient E. colistrain. Similar results have been described for the cloned pstIR and taqIR genes (10, 34). Since we found partial activity of R. MthT at 37°C, E. coli must contain efficient mechanisms to prevent cleavage by R. MthTI or to repair cleaved DNA. This protection appears not to be complete, since only low amounts of pURM4\(DM\) DNA could be isolated and appeared to be partially degraded.

The thermophilic methanogens M. thermoformicicum and M. thermoautotrophicum are related species (40). It has been shown that M. thermoautotrophicum and other thermophilic bacteria contain low levels of  $m^5C$  (8). This has been explained by the fact that those organisms avoid production of  $m^5C$  because high temperatures favor deamination of  $m^5C$  ( $m^5C \rightarrow T$ ), which would result in a point mutation (8). The presence of an  $m^5C$ -MTase in M. thermoformicicum THF suggests the presence of a mechanism either to avoid deamination of  $m^5C$  or to repair mismatched DNA.

Since M. thermoformicicum is a thermophilic organism, it was not unexpected to find that its MthTI system showed activity at 65°C, the optimal growth temperature of the host. In fact, we found that R. MthTI is highly active even at temperatures up to 75°C (unpublished results). All other R/M systems encoding an m<sup>5</sup>C-MTase have been isolated from mesophilic organisms (45). The observation that R.MthTI and M.MthTI enzymes extracted from E. coli could be assayed at high temperatures in standard buffer systems indicates that the thermostability of the MthTI enzymes is an intrinsic property. In the absence of a three-dimensional structure, comparison of primary sequences derived from homologous mesophilic and thermophilic proteins may give some indications as to the basis for thermostability. In general, thermostability of proteins can be attributed to an increased conformational stability. This may be realized by interactions between different parts of the protein, mediated by hydrophobic, electrostatic, or other interactions, that prevent denaturation at high temperatures (11). Notably, two kinds of differences which could contribute to such interactions were observed when the protein sequences of the MthTI system were compared with those of their mesophilic counterparts (Fig. 5 and 6). Both R.MthTI and M.MthTI showed a shift of charged amino acid residues from the N-terminal to the C-terminal part of the protein

compared with the other enzymes, whereas the overall charge of the proteins remained the same. In addition, single amino acid substitutions in conserved regions of M.MthTI tend to be less polar residues.

The M.MthTI enzyme shares extensive amino acid similarity with the other GGCC-recognizing monospecific MTases M. NgoPII and M. HaeIII in conserved regions that are expected to be involved in substrate binding and recognition of the target sequence (19, 26) and methyl group transfer (6). This finding supports the conclusions drawn from analyses of several other R/M systems that the C-MTases seem to have evolved from a common origin (18). In contrast, ENases, even those with same sequence specificity, are usually different, indicating different evolutionary origins. The MthTI system is an exception, since R.MthTI showed a high degree of similarity to R. NgoPII isolated from N. gonorrhoeae. R.MthTI and R.NgoPII are similar in size and are encoded by genes that have the same orientation with respect to the corresponding MTase gene. The same organization and homology to the NgoPII system was reported for the isospecific R/M system FnuDI from Fusobacterium nucleatum D, but unfortunately its sequence has not been published (45). In contrast, the R. Hae III protein sequence did not show similarities to that of R. NgoPII and thus is probably also different from the R.MthTI protein sequence, in accordance with the different organization of the HaeIII R/M system (45).

The high similarity at the protein and DNA levels and the identical organizations of the MthTI and NgoPII R/M systems strongly suggest that the entire systems have been derived from a common ancestor and disseminated via horizontal gene transfer. Since M. thermoformicicum belongs to the domain Archaea and N. gonorrhoeae belongs to the domain Bacteria, this conclusion implies that gene transfer had occurred between these evolutionarily different groups of prokaryotes (46). If so, it is reasonable to assume that the direction of transfer is from the thermophilic M. thermoformicicum to the mesophilic N. gonorrhoeae rather than vice versa, since the MthTI system is also active at low temperatures and would immediately confer a selective advantage when transferred to a mesophilic host. This is not to be expected when an R/M system from a mesophilic bacterium is introduced into a thermophilic organism. Among the possible avenues for gene transfer, transformation by DNA released into the environment is a likely one, especially since N. gonorrhoeae shows a natural competence for DNA uptake (5). Conjugation, however, cannot be excluded since it is known to play a significant role in gene transfer between distantly related organisms, including prokaryotes and eukaryotes (21). It is tempting to speculate that the plasmid location of the MthTI system in M. thermoformicicum THF has been involved in the presumed transfer.

Comparison of the MthTI and NgoPII systems at the nucleotide level revealed that the high level of sequence identity did not extend beyond the coding regions of the ENase and MTase genes and could reflect the requirement for appropriate, host-specific expression signals, which are known to be very different between members of the Archaea and Bacteria (4).

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Identification of the CTAG-recognizing restriction-modification systems *Mth*ZI and *Mth*FI from *Methanobacterium thermoformicicum* and characterization of the plasmidencoded *mthZIM* gene

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# Identification of the CTAG-recognizing restrictionmodification systems *MthZI* and *MthFI* from *Methanobacterium thermoformicicum* and characterization of the plasmid-encoded *mthZIM* gene

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### **ABSTRACT**

Two CTAG-recognizing restriction and modification (R/M) systems, designated MthZI and MthFI, were identified in the thermophllic archaeon Methanobacterium thermoformicicum strains Z-245 and FTF, respectively. Further analysis revealed that the methyltransferase (MTase) genes are plasmid-located in both strains. The plasmid pFZ1-encoded mthZiM gene of strain Z-245 was further characterized by subcloning and expression studies in Escherichia coli followed by nucleotide sequence analysis. The mthZIM gene is 1065 bp in size and may code for a protein of 355 amino acids (M, 42,476 Da). The deduced amino acid sequence of the M.MthZI enzyme shares substantial similarity with four distinct regions from several m4Cand moA-MTases, and contains the TSPPY motif that is so far only found in m4C-MTases. Partially overlapping with the mthZiM gene and in reverse orientation, an additional ORF was identified with a size of 606 bp potentially coding for a protein of 202 amino acids (M, 23.710 Da). This ORF is suggested to encode the corresponding endonuclease R.MthZI.

## INTRODUCTION

Restriction and modification (R/M) systems are widespread among prokaryotes (1) and have been identified in about 25% of the presently examined species (2). Their major function is proposed to be the protection from contamination by DNA of foreign origin, particularly derived from bacteriophage infection (3). The most common R/M systems are those of the type II, consisting of two enzymatic activities, an endodeoxyribonuclease (ENase) and a DNA-methyltransferase (MTase), which both recognize an identical short DNA sequence (2). Genetic characterization of type II R/M systems have shown that the ENase and MTase genes most often are closely linked (2, 4).

Three types of MTases, forming different methylation products, can presently be distinguished: those generating 5-methylcytosine ( $m^5C$ ), N4-methylcytosine ( $m^4C$ ), and N6-methyladenine ( $m^6A$ ) (2). Based on their amino acid similarities, those MTases can be grouped into two families, the  $m^5C$ - on the one and the  $m^4C$ - and  $m^6A$ -producing MTases on the other hand (5-9). In contrast to the MTases, ENases usually do not share significant similarities on protein sequence level, except for some isoschizomeric enzymes (10-12).

The thermophilic methanogen Methanobacterium thermoformicicum belongs to one of the three fundamentally different groups of living organisms, the domain Archaea, distinguished from the Bacteria and the Eucarya by various unique characteristics (13, 14). Several strains of the species M.thermoformicicum were found to harbor partially homologous plasmids (15). One of these plasmids, plasmid pFV1, carries the genes for the GGCC-specific MthTI R/M system of M.thermoformicicum strain THF (12). In the present report, we describe the identification of two CTAG-recognizing R/M systems, designated MthZI and MthFI, in M.thermoformicicum strains Z-245 and FTF, respectively, and the characterization of the plasmid-encoded mthZIM gene.

## **MATERIAL AND METHODS**

## Bacterial strains, vectors, and growth conditions

M.thermoformicicum strains Z-245 (DSM 3720), FTF (DSM 3012), THF (DSM 3848), SF-4 (K. Yamamoto, Osaka City University, Japan), FF1 (15), FF3 (15) and CSM3 (16) were cultivated on  $H_2/CO_2$  as the sole carbon and energy source as described previously (15). Escherichia coli strains DH5 $\alpha$  (Life Technologies) and HB101 (17) were used for subcloning and propagation, respectively, of derivatives of plasmids pUC18 and pUC19 (18). E.coli TG1 (19) served as host strain for phages M13mp18 and M13mp19 (18). The E.coli strains were routinely grown in L-broth (20) at 37°C. If appropriate, ampicillin (50 µg/ml), isopropyl- $\beta$ -D-thiogalactopyranoside (1 mM), or 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactoside (0.004%) was added to the culture medium.

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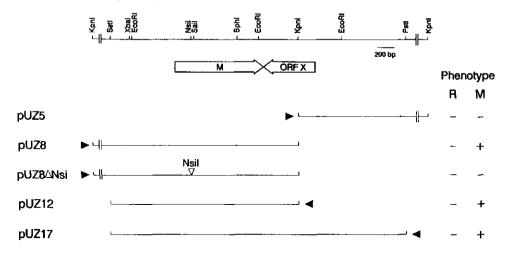


Figure 1. Restriction map and subclones of two adjacent *Kpn*1 fragments (6.1 kb) of plasmid pFZ1. The orientation and location of the *mthZIM* gene (M) and ORF X are indicated. The *in vivo* ENase (R) and MTase (M) activity of the subclones are indicated on the right side; (\*\*) denote the location of the *lac*Z promoter of the vector part.

### DNA manipulations and sequence analysis

Restriction endonuclease MaeI was used as recommended by the supplier (Boehringer Mannheim, Germany). All other restriction enzymes. T4 DNA ligase and Klenow DNA fragment were purchased from Life Technologies Inc. (Gaithersburg, Md.). DNA manipulations in *E.coli* were performed following established procedures (20). Total DNA was isolated from M.thermoformicicum as described previously (15). For nucleotide sequence determination, DNA fragments were isolated from agarose gels using a Geneclean kit as described by the supplier (Bio 101, La Jolla, Calif.) and subcloned into M13mp18/19. The nucleotide sequences of overlapping fragments of both strands were determined by the dideoxy chain termination method (21) with the Sequenase kit according to the recommendations of the supplier (United States Biochemical Corp. Cleveland, Ohio).  $[\alpha^{-32}P]dATP$  (110 TBq/mmol) was purchased from Amersham (UK). Computer analysis of the sequence data was done with the GCG package version 6.0 (22) and the CAOS/CAMM facilities at Nijmegen. The Netherlands.

#### MthZI plasmid constructions

Plasmids pUZ5 and pUZ8 (Fig. 1) were derivatives of pUC19 which contain *Kpn*I-fragments of 2.1 kb and 3.7 kb, respectively, derived from plasmid pFZ1 from *M.thermoformicicum* strain Z-245 (15). Plasmid pUZ8ΔNsi (Fig. 1) was constructed by digestion of pUZ8 with *Nsi*I followed by treatment for 30 min with Klenow DNA polymerase in the presence of all four dNTPs (2 mM each) to remove 3'-overhanging ends. After ligation the DNA was used to transform *E.coli* HB101 cells. The resulting frameshift mutation in plasmid pUZ8ΔNsi was confirmed by restriction and sequence analysis (data not shown).

Several attempts failed to directly clone the 3.6 kb Sstl-Pstl fragment from plasmid pFZ1 (Fig. 1) into pUC18/19. Therefore, a plasmid that carries this fragment containing the mthZIM gene

and open reading frame X (ORF X) was constructed on the basis of cloned pFZ1 DNA. For this purpose, pUZ5 and a derivative of pUZ8, which contained the 3.7 kb KpnI-insert in opposite orientation relative to the pUC19-located lacZ-promoter, were used. For some manipulations, sites present in the polylinker of the vector parts were employed. First, a 2.3 kb Sstl-HindIII fragment of plasmid pUZ8 was cloned into pUC18 digested with SstI and HindIII to yield plasmid pUZ12 (Figure 1). A short fragment of the polylinker located at the 5'-site of the truncated ORF X was removed from plasmid pUZ12 by digestion with Smal and Pstl. Subsequently, a 1.2 kb Smal-Pstl fragment containing the 5'-part of the ORF X gene was isolated from plasmid pUZ5 and inserted into the digested pUZ12 resulting in plasmid pUZ15. Due to this cloning strategy, which was chosen to avoid a possible lethal effect of transforming E.coli with a plasmid carrying an intact ORF X, plasmid pUZ15 harbors an ORF X that contains a frameshift mutation caused by a 14 bp KpnI-Smal-KpnI polylinker fragment. Digestion of plasmid pUZ15 with KpnI removed the 14 bp fragment and religation restored wild-type sequence in the pFZ1-derived insert DNA. resulting in plasmid pUZ17 (Figure 1). The integrity of the pFZ1 DNA at this location in pUZ17 was confirmed by sequence analysis (data not shown).

## Preparation of cell-free extracts

Approximately 0.1 g frozen cells of *M.thermoformicicum* strain Z-245 or FTF were resuspended in 0.5 ml lysis buffer (0.1 M NaCl, 0.01 M EDTA, 0.01 M  $\beta$ -mercaptoethanol and 0.05 M Tris-HCl pH 7.6) and disrupted by sonication. After centrifugation for 2 min at 15000×g, the supernatant, which contained about 3.5 to 5.0  $\mu$ g protein/ $\mu$ l, was collected, mixed with 1 vol glycerol and stored at  $-20^{\circ}$ C before use. The extracts were found to be stable for at least 12 month without loss of the R/M activities.

#### Analysis of the MthZI and MthFI ENase and MTase activities

The in vitro activities of the MthZI and MthFI systems were assayed essentially as described previously (12) with extracts prepared from M. thermoformicicum strains Z-245 and FTF. The buffer used under ENase conditions contained 0.1 M NaCl, 0.2 M KCl, 0.01 M MgCl<sub>2</sub>, 0.001 M dithioerythritol and 0.05 M Tris-HCl pH 7.6. As methyl-group donor 0.8 mM Sadenosylmethione (AdoMet) was used under MTase conditions. All assays were performed at 55°C. When specified, the ENase assays were deproteinized prior to agarose gel electrophoresis by incubation with proteinase K (0.1 mg/ml; Boehringer GmbH, Mannheim, Germany) in the presence of 0.5% sodium dodecyl sulfate for 15 min, followed by extraction with phenol/chloroform. Subsequently, the DNA was precipitated with ethanol and resuspended in ENase buffer. As substrate for the R/M enzymes, phage λ DNA and plasmid pUZ3, consisting of a 6.5 kb Smal-fragment of plasmid pFZ1 from M.thermoformicicum strain Z-245 (15) cloned into pUC19, were used.

#### Primer extension

Primer extension was carried out as described previously (12). DNA from plasmid pUV1 that consists of a completely sequenced, 7.4 kb Xhol-Ssfl fragment of plasmid pFV1 from M.thernoformiccum strain THF cloned into pUC19 (12, 16), was digested with R.MthZI or R.MaeI and used a template for extension of a primer (5'-CTGTAGTTCAGGATC) that binds to position 375 to 361 of the insert of pUV1.

## RESULTS

## Identification of the MthZI and MthFI R/M systems

Following the characterization of the plasmid-encoded restrictionmodification system MthTI from M. thermoformicicum strain THF (12) we also analyzed other thermophilic members of the genus Methanobacterium for the presence of ENase activity (Table 1). Extracts prepared from M.thermoformicicum strains Z-245 and FTF, incubated with phage λ- or plasmid pUZ3 DNA under ENase conditions, were found to produce discrete DNA fragments indicating the presence of site-specific ENase activity (Figure 2A). Identical DNA patterns were derived from ENase activity of strains Z-245 and FTF, which was designated R. MthZI and R.MthFI, respectively. In addition, in vitro methylation assays showed that the cell-free extracts of both strains exhibit AdoMet-dependent MTase activity that generated at least partially modified pUZ3 DNA (Figure 2A, lanes 9-12). Since this DNA methylation affects the ENase activities of strain Z-245 and FTF, it follows that the DNA is modified by the corresponding MTases M.MthZI and M.MthFI, respectively. To verify the in vivo activity of both MTases, total DNA isolated from M.thermoformicicum strain Z-245 or FTF was incubated with extracts prepared from either strain. Figure 2B illustrates that DNA from strains Z-245 and FTF was resistant to digestion with R.MthZI (lanes 2, 3) but not with R.KpnI which was used as a control (lanes 4,5). Similar results were observed using R.MthFI (data not shown). The resistance of DNA from strain Z-245 and FTF to digestion with ENase from either strain confirmed the in vivo activity of M.MthZI and M.MthFI. In contrast, DNA isolated from strain THF, which carries the GGCC-recognizing MthTI system (12), was sensitive to R.MthZI

Table 1. Distribution of plasmid DNA and ENase activity in M.thermoformicicum

Strain	Plasmid (kb)	Recognition sequence of ENase activity	Reference	
Z-245	pFZ1 (11.0)	CTAG	This work	
FTF	pFZ2 (11.0)	CTAG	This work	
THF FF1, FF3,	pFV1 (13.5)	GGCC	(12)	
CSM3, SF-4	_	_	This work	

(Figure 2B, lane 1). These results indicate that *M.thermoformicicum* strains Z-245 and FTF each harbor a R/M system, designated *MthZI* and *MthFI*, respectively, with identical sequence specificity.

## Sequence specificity of R.MthZI and R.MthFI

In order to determine the recognition sequence of R.MthZI and R.MthFI we compared the restriction patterns produced by these ENases with those produced by several commercially available ENases. We identified the CTAG-recognizing ENase R. Mael as an isoschizomer of R.MthZI and R.MthFI since it generates restriction patterns identical to that produced by the M. thermoformicicum enzymes using phage  $\lambda$ - or plasmid pUZ3 DNA as substrate (Figure 2A, lanes 2-4 and 6-8). For some of the restriction fragments generated by digestion with extracts from the M. thermoformicicum strains, slightly aberrant mobilities were observed if samples were not deproteinized before gel electrophoresis, i.e. large fragments show an increased and small fragments a decreased mobility (see Figure 2A, lanes 1 and 5 for results with Z-245 extract). This most likely is due to components in the extracts with similar properties as the histonelike DNA binding protein HMt from M.thermoautotrophicum strain AH (23).

Since both R/M systems MthZI and MthFI recognize the same target sequence, MthZI from strain Z-245 was used for a more detailed analysis. The exact cleavage position of R.MthZI was determined by primer extension experiments. The extension products of R.MthZI and R.MaeI digested DNA had identical sizes (Figure 3). Considering that the 5'-overhanging ends generated by both ENases were filled up by Klenow DNA polymerase and therefore the 3'-nucleotide of the extension products represent the 5'-nucleotide of the cleavage sites, comparison of the extension products with the parallel run sequence ladder revealed that both ENases cleave the target sequence to yield C\daggerTAG.

## Identification of the mthZIM gene

M.thermoformicicum strain Z-245 and FTF harbor identical or nearly identical plasmids, pFZ1 and pFZ2, respectively, which are partially homologous to plasmid pFV1 isolated from strain THF (15). Since the R/M system MthTI of strain THF is located on plasmid pFV1 (12) and no ENase activity was detected in extracts prepared from other M.thermoformicicum strains that lack plasmid DNA (Table 1), we anticipated that the R/M system MthZI of strain Z-245 could be located on plasmid pFZ1. To study this possibility, cloned plasmid pFZ1 DNA was tested for in vivo modification by incubation with Z-245 extract and subsequent analysis on agarose gel. All plasmids containing pFZ1 DNA were sensitive to R.MthZI except one, pUZ8, which was only partially digested with R.MthZI despite the presence of

multiple R.MthZI sites in at least the vector part of pUZ8. The protection against digestion with R. MthZI was even higher when E. coli HB101 was used to propagate plasmid pUZ8 (Figure 2B, lane 7). In addition, we tested pUZ8 DNA for sensitivity to R. Xbal since its target sequence TCTAGA includes the CTAG site recognized by R.MthZI. Sequence analysis (see below) showed that pUZ8 contains two R. Xbal restriction sites, one in the insert and one in the vector part. Plasmid pUZ8 was-in contrast to other plasmids tested-partially resistant to digestion with R. XbaI (Figure 2B, lane 11). In contrast, plasmid pUZ8\(Delta\)Nsi, which contains a frameshift mutation, was found to be sensitive to digestion with both R.MthZI and R.XbaI (Figure 2B, lanes 8, 12). These results indicate that pUZ8 encodes a MTase activity which modifies the R. MthZI and the R. Xbal recognition sites. Subcloning of pUZ8 DNA followed by R.MthZI digestion allowed the location of the mthZIM gene on a 2.3 kb Sstl-KpnI fragment, contained in plasmid pUZ12 (Figure 1). Although the in vivo modification of DNA containing the mthZIM gene clearly showed that this gene is functionally expressed in E.coli, no activity of M.MthZI was observed in in vitro assays performed as described earlier (12).

Sequence analysis (see below) revealed that the insert of pUZ12 contained, in close proximity to the mthZIM gene, part of an open

reading frame (ORF X) which is a good candidate for the corresponding mthZIR gene. To exclude the possibility that the ENase gene is truncated in pUZ12 we constructed plasmid pUZ17 that contain the mthZIM gene and the entire ORF X (Figure 1). However, neither in vitro using cell-free extracts nor in vivo in restriction assays using bacteriophage  $\lambda$ . ENase activity was observed with E.coli HB101 harboring either plasmid pUZ17 or pUZ12 (data not shown).

### Nucleotide sequence of the mthZIM gene

The complete nucleotide sequence of the 3561 bp \$st1-Pst1 insert of plasmid pUZ17 has been determined. Analysis of the sequence revealed two large, converging and partially overlapping ORFs. The first ORF contains an ATG start codon at position 779 which is preceded by a potential ribosome binding site (RBS; position 770 through 775), and a TAG stop codon at position 1844. It could code for a polypeptide of 355 amino acids (Mr, 42,476 Da). Since plasmids containing this ORF were resistant to digestion with R.MthZI but became sensitive to this ENase when a frameshift mutation was introduced (pUZ8\Delta\ni), we conclude that it represents the mthZIM gene. The second ORF, designated ORF X, is located on the complementary strand and ranges from position 2488 to the termination codon TAA at position 1837.

A

s 1 2 3 4 5 6 7 8 9 10 11 12 13



В

s 1 2 3 4 5 6 7 8 9 10 11 12 13 14 s



Figure 2. In vitro (A) and in vivo (B) activities of the MihZI and MihFI R/M systems. (A) Lanes 1–8, ENase assays using extracts prepared from strain Z-245 (lanes 1, 5, not purified, lanes 2, 6, deproteinized), FTF (lanes 3, 7, deproteinized) and 5 Units R. Mael (lanes 4, 8) with phage A DNA (lanes 1–4) and pUZ3 DNA (lanes 5–8) as substrate; lanes 9–12, pUZ3 DNA incubated under MTase assay conditions with Z-245-extract (lanes 9, 11) and FTF-extract (lanes 10, 12), with (lanes 9, 10) and without AdoMet (lanes 11, 12) followed by digestion with R. MihZI (lanes 9, 11) and R. MihFI (lanes 10, 12). Lane 13, undigested plasmid pUZ3 DNA (1 µg). Lane s, size marker phage \(\lambda\) DNA (0.7 µg) digested with R. HindIII. (B) Lanes 1–5, about 0.5 µg total DNA isolated from M. thermoformicicum strain THF (lane 1), Z-245 (lanes 2, 4) and FTF (lanes 3, 5) incubated under ENase conditions with extract prepared from strain Z-245 (lanes 1–3) and R. KpnI (lanes 4, 5). Lanes 7–14, about 1.0 µg plasmid pUZ8 (lanes 7, 9, 11, 13) and pUZ8\(\text{NSi}\) DNA (lanes 8, 10, 12, 14) incubated under ENase conditions with extract prepared from strain Z-245 (lanes 7, 8), R. Mael (lanes 9, 10), R. XboI (lanes 11, 12), and R. KpnI (lanes 13, 14). Lane 6, undigested plasmid pUZ8 DNA (1.0 µg). Lane s, size marker phage \(\lambda\) DNA (0.7 \(\text{\text{pl}}\) gidested with R. HindIII.

A potential start codon (GTG at position 2443) is preceded by a sequence that may serve as RBS (position 2454 through 2449). If the GTG is used, the ORF X encodes a protein of 202 amino acids with a calculated molecular mass of 23,710 Da.

The regions flanking the *mthZIM* gene and ORF X were analyzed for archaeal transcription signals. Within an AT-rich 250 bp region preceding the *mthZIM* gene, that contains several direct repeats, various DNA stretches with similarities to the essential TATA box of archaeal promoters could be identified (24, 25). Inspection of the upstream region of the ORF X revealed no obvious promoter-like sequences. Downstream of *mthZIM* and ORF X, a conserved archaeal transcription termination signal consisting of a T-rich stretch (26) was identified.

## Protein sequence comparisons

The deduced amino acid sequence of the M. MthZI protein was compared to that of known sequences of other MTases. No significant homology was observed with MTases that produce m<sup>5</sup>C. M. MthZI shares, however, similarities with distinct

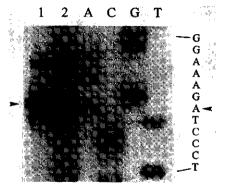


Figure 3. Primer extension analysis of the R.Mth/ZI cleavage-site. Plasmid pUV1 DNA, digested with R.Mael (lane 1) and R.Mth/ZI (lane 2), respectively, was used as template for extension of the primer. Arrows indicate the major extension product and its corresponding nucleotide derived from incubation with both ENases. A shorter extension product attributed to a specific termination is also present. A DNA sequence ladder run in parallel is shown at the right.

regions from several m<sup>4</sup>C- and m<sup>6</sup>A-MTases. The MTases showing the highest similarity with M.MthZI include M.BamH2 (27), M.BamH1 (9), M.Smal (28) and M.Cfr91 (7), all of which were proven or assumed to be m<sup>4</sup>C-MTases, and two representatives of the m<sup>6</sup>A-MTase family, M.Hinfl (29) and M.Rsrl (30). Four blocks with conserved amino acid motifs, similar to those reported by Brooks et al. (1991), could be identified (Figure 4). The longest conserved segment, block D, contains the FXGXG-motif (motif DII in Figure 4; X = variable amino acid) common to almost all MTases (6-8). Block B contains the (S/D)PP(Y/F) motif which is present in all m<sup>6</sup>A-and m<sup>4</sup>C-MTases (7, 9, 31). Block A is less conserved in M.MthZI but is, similar to other m<sup>6</sup>A- and m<sup>4</sup>C-MTases, located at the N-terminus and contains the characteristic DXXE motif

In addition to the conserved amino acid motifs identified by Brooks et al. (1991), the protein sequence comparison data revealed two other amino acid regions, which were found to be conserved in all m<sup>4</sup>C-MTases (7, 27, 28, 32), except for M.Mval (7), and in several m<sup>6</sup>A-MTases such as M.Hinft (29; Figure 4). Both regions are flanking the FXGXG motif (DII). One region, DI, contains the motif (P/S)XX(L/M)Y (Y = hydrophobic, non aromatic) and is located 22 amino acids N-terminal from the sequence FXGXG, whereas motif DIII, RXX(I/V)(G/S)XEX<sub>11</sub>(R/K), is located 11 amino acids C-terminal from the FXGXG sequence. This latter motif contains three highly conserved charged residues.

Comparison of the amino acid sequence deduced from ORF X revealed no significant homology with other protein sequences found in the data base.

## DISCUSSION

This report describes the identification of two novel R/M systems with the same sequence specificity, *MthZI* and *MthFI*, from the archaeon *M.thermoformicicum*. In addition, the characterization of the first CTAG-recognizing methyltransferase, M.*MthZI*, is presented. Both *MthZI* and *MthFI* R/M systems are produced by two plasmid-harboring strains, Z-245 and FTF, respectively. Further analysis revealed that the *mthZIM* gene is located on the 11 kb plasmid pFZI of strain Z-245 (15). Since the plasmids

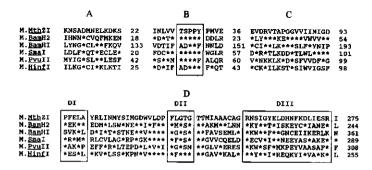


Figure 4. Local amino acid sequence alignment of M. MthZl and other DNA methyltransferases. Amino acid sequences of four conserved regions (A-D) from M. MthZl, M. BamHZ, M. BamHZ, M. BamHZ, M. BamHZ, M. BamHZ, M. Smal, M. Putll and M. Hinfl are shown. Region D is subdivided into three conserved amino acid blocks (DI-DIII). Residues identical to those in M. MthZl are denoted by asterisks. Amino acid motifs mentioned in the text are blocked. Numbers at the end of each line indicate the position of the last amino acid in the region.

pFZ1 and pFZ2 of the strains Z-245 and FTF are highly similar (15), it is very likely that the M. MthFI enzyme is also encoded by plasmid pFZ2. Indeed, pFZ2 DNA showed strong hybridization with the mthZIM gene as probe (data not shown). In addition to the GGCC-specific, plasmid-located MthTI system of strain THF (12), the MthZI and MthFI systems represent another class of plasmid-encoded R/M systems in M.thermoformicicum. Since no ENase or MTase activity could be detected in other M. thermoformicicum isolates that appeared to be plasmid-free (Table 1), this would suggest that the occurrence of R/M systems in these methanogenic Archaea depends on the presence of extrachromosomal DNA elements.

Extracts prepared from M.thermoformicicum strains Z-245 and FTF contained high ENase and low MTase activities. The cloned mthZIM gene could be functionally expressed in E. coli as shown by in vivo modification of vector DNA carrying the complete mthZIM gene. No activity was, however, detected in in vitro MTase assays using extracts prepared from different E.coli strains with the mthZIM gene in either orientation with respect to the lacZ promoter of the vector. Since the in vitro MTase conditions used worked adequately with extracts prepared from the methanogenic hosts, a low expression level of the mthZIM gene or instability of the M. MthZI protein in E. coli could explain the inability to detect in vitro activity.

Comparison of the deduced amino acid sequence of the M.MthZI protein revealed four regions with significant similarity to m<sup>4</sup>C- and m<sup>6</sup>A-MTases but not to m<sup>5</sup>C-MTases (Figure 4). Sequence comparisons did not reveal motifs that would allow a clear discrimination between m<sup>4</sup>C- and m<sup>6</sup>A-MTases. However, the deduced protein sequence of M. MthZI contains the TSPPY motif which so far has only been found in m4C producing MTases (7, 28, 29, 32).

The recognition sequence CTAG of MthZI and MthFI forms the core of the sequence TCTAGA, the target of the XbaI R/M system. We observed that DNA is protected to a similar extent against cleavage by either R. XbaI or R. MthZI when it is methylated by M. MthZI. If M. MthZI is a m4C-MTase, it would modify the XbaI-site to yield Tm4CTAGA. Alternatively, if M.MthZI generates m6A, it would modify the Xbal-site to yield TCT<sup>m6</sup>AGA. Either modification pattern of the XbaI-site would be, in addition to the three already described (33, 34), a fourth one that prevent cleavage by R.XbaI.

Partially overlapping with the mthZIM gene and in opposite orientation, another ORF, ORF X, was identified. Although we have no direct evidence, ORF X could well represent the corresponding mthZIR gene. In favour of this possibility are the findings that (i) ENase and MTase genes most often are closely linked (2), (ii) the size of the protein encoded by ORF X is similar to that of other ENases, (iii) the mthZIM gene and ORF X constitute a 1.9 kb module in plasmid pFZ1 that is absent in plasmid pFV1, which in turn contains at this location a unique fragment encoding the MthTI R/M system of strain THF (12, 16), and (iv) no ENase activity was observed in other, closely related strains of M. thermoformicicum that lack plasmid DNA (Table 1). The failure of detecting the expected ENase activity in E.coli might be ascribed to a low expression level of ORF X because of its unusual start codon GTG (35).

Among the large number of identified R/M systems (1) only four have previously been found to recognize the same sequence as MthZI and MthFI (1, 2, 36, 37) indicating that CTAG is a rarely occurring target. Two of those systems, MaeI and MjaI, were identified in the methanogens Methanococcus aeolicus (36) and Methanococcus jannaschii (1). This suggest that, together

with the here described MthZI and MthFI, R/M systems recognizing CTAG are more common in Archaea than in Bacieria.

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## Summary and concluding remarks

The identification of the Archaea as a third primary lineage of life and their adaptation to extreme environmental conditions have generated considerable interest in the molecular biology of these organisms. Most progress in the investigation of archaeal mobile genetic elements, i.e. viruses, plasmids and insertion sequences, has been made in the halophilic branch while only limited knowledge was available about mobile elements of methanogens (reviewed in Chapter 1). The aim of this thesis was therefore to get more insight into the molecular genetics of mobile elements from methanogens. Thermophilic species of the genus Methanobacterium were used as model organisms in this study, since they are among the best characterized methanogens.

Phylogenetic studies of the species M.thermoformicicum and strains of M.thermoautotrophicum are described in Chapter 2. The comparison of two variable 16S rRNA regions allowed the conclusions that (i) M. thermoformicicum consists of two groups of strains, the Z-245-group (including strains Z-245, FTF, THF, FF1, FF3 and CSM3) and the CB12-group (consisting of the strains CB12, SF-4, and HN4), which probably constitute different species. (ii) M.thermoautotrophicum  $\Delta H$  is closely related to the Z-245-group, and (iii) M.thermoautotrophicum Marburg belongs to neither group and most likely represents a different species (Table 1). This classification of M.thermoformicicum and M.thermoautotrophicum strains obtained by comparative 16S rRNA analysis is in line with recently reported results derived from DNA-DNA hybridization studies (8). Both approaches are based on genotypic characters which generally are more reliable for the determination of phylogenetic relationships than classical phenotypic ones. Therefore, the proposed reclassification of the examined thermophilic Methanobacterium strains may reflect their phylogeny more accurately than the current classification. Moreover, some other characters of the examined methanogens including genetic fingerprints with fdhA (Chapter 2 and 4), the sensitivity to phage  $\Phi$ F1 (Chapter 3) and the distribution of FR-I (Chapter 6) provide additional evidence for the proposed new taxonomy of M. thermoformicicum and M. thermoautotrophicum (Table 1). Another phylogenetically relevant aspect reported in Chapter 2 was the finding that the non-formate utilizers M. thermoautotrophicum AH and Marburg contain sequences similar to the fdhA and fdhB genes from M. formicicum. The presence of fdhAB-like sequences in strain AH and Marburg suggest that both M. thermoformicicum and M. thermoautotrophicum are descendants of a common formate-utilizing ancestor.

It has recently been shown that *M.thermoautotrophicum*  $\Delta H$  and Marburg differ clearly in their genome size (1.725 versus 1.623 kb, respectively) and the position of restriction sites in the chromosomal DNA for the endonucleases *Not*I, *Pme*I and *Nhe*I (7). These findings are likely to reflect the limited homology of both *M.thermoautotrophicum* strains on the genomic level. Similarly, also strain  $\Delta H$  and *M.thermoformicicum* THF have been found to differ considerably in genome size (1.725 versus 1.600 kb, respectively) and *Not*I restriction pattern (7). This would contradict the results obtained by DNA-DNA similarity studies and comparative 16S rRNA sequence analysis which indicate a close relationship of these two strains (Chapter 2). However, the results of the genomic analysis of strain THF have to be

interpreted with caution for two reasons. Firstly, the *Not*I-site (5'-GCGGCCGC) comprises the target site of the GGCC-recognizing restriction-modification system *Mth*TI harbored by strain THF (see Chapter 7). As the consequence, the methyltransferase of the *Mth*TI system probably modifies the *Not*I-sites contained in DNA from strain THF to yield 5'-GCGG<sup>ne</sup>CCGC which is resistant against cleavage by *Not*I (4). The reported two *Not*I restriction fragments of 1.350 and 250 kb generated from THF DNA (7) may therefore not reflect the real number of *Not*I-sites in the chromosome of strain THF. Secondly, the enormous size of the large *Not*I fragment probably does not allow an accurate determination of its size.

Table 1. Classification of thermophilic Methanobacterium strains

Organism		Plasmid (kb)	Homology with		Phage sensitivity		Homology <sup>e</sup> group
			FR-I FR-II		FR-II <b>Φ</b> F1		
M.thermoformicicum	CB12		_	_	_	_	CB12
-	SF-4	_	_	_	_	_	CB12
	HN4	_	_	+	_	_	CB12
	Z-245	pFZ1 (11.0)	+	_	+	_	Z-245
	FTF	pFZ2 (11.0)	+	_	+	_	Z-245
	THF	pFV1 (13.5)	+	+		_	Z-245
	FF1		+	_	+	_	Z-245
	FF3	<del></del>	+	_	+	+	Z-245
	CSM3	_	+	+	+	_	Z-245
1.thermoautotrophicus	n ΔH	_	+	_	+	_	Z-245 <sup>b</sup>
•	Marburg	pME2001 (4.4)	_	_	_	_	Marburg <sup>b</sup>

Based on DNA-DNA similarity, 16S rRNA signature and genetic fingerprint with fdhA.

Chapter 3 describes the characterization of the novel archaeal phages  $\Phi F1$  and  $\Phi F3$  that are able to infect several thermophilic strains of *Methanobacterium* (Table 1). Both phages differ with respect to their host range and the topology of their double-stranded DNA genomes. While phage  $\Phi F1$  has a broad host range and contains a linear, approximately 85-kb genome,  $\Phi F3$  was specific for *M.thermoformicicum* FF3 and contained a circular, approximately 36-kb genome. No similarity was found between the genomes of  $\Phi F1$  and  $\Phi F3$  nor between both phages and genomic DNA from different *Methanobacterium* strains or from phage  $\psi M1$  of *M.thermoautotrophicum* Marburg.

The isolation and initial molecular analysis of three plasmids, pFV1 (13.5 kb), pFZ1 (11.0 kb) and pFZ2 (11.0 kb), harbored by *M.thermoformicicum* strains THF, Z-245 and FTF, respectively, is reported in Chapter 4. Using cloned pFZ1 DNA as hybridization probe, the plasmids were found to constitute a family of highly related elements. Whereas pFZ1 and pFZ2 are probably identical, only partial similarity was observed between pFZ1 and pFV1. Furthermore, genetic fingerprinting experiments using *fdhA* from *M.formicicum* as hybridization probe allowed a subdivision of the species *M.thermoformicicum* into the CB12-group and the Z-245-group, comprising among others the plasmid-harboring strains Z-245, FTF and THF (Table 1).

b Unique hybridization pattern obtained with fdhA.

The relatedness of the plasmid DNA was confirmed by sequence analysis of pFV1 and pFZ1 (Chapter 5). Comparison of the primary sequence of pFV1 (13513 bp; see also Appendix A) and pFZ1 (11014 bp; see also Appendix B) revealed a modular organization of the plasmid genomes: a backbone structure, conserved on the sequence level and in overall gene order, which is interspersed with plasmid-specific elements. The organization of the *M.thermo-formicicum* plasmids resembles that of prokaryotic chromosomes both of which are subjected to DNA rearrangements, in particular insertions and/or deletions, thereby retaining a basic genome organization. The high sequence similarity and the comparable genetic maps suggest that pFV1 and pFZ1 (and pFZ2) have originated from a common ancestor. If so, the plasmids probably share homologous functions necessary for plasmid replication and maintenance which should be located within regions with high interplasmid similarity, i.e. the plasmid backbone. Those essential functions may include two large palindromic regions and a putative gene encoding a NTP-binding protein which are contained within the conserved backbone structure. In contrast, the plasmid-specific sequence blocks probably represent accessory elements which do not specify essential plasmid functions.

Both plasmids pFV1 and pFZ1 harbor sequences with similarity to chromosomal DNA of different thermophilic methanogens (Chapter 6). One of those, named FR-I, represents an accessory element of pFV1 with chromosomal counterparts in several *M.thermoformicicum* strains and *M.thermoautotrophicum* ΔH (Table 1). Comparison of the plasmid-derived and chromosomal FR-I elements revealed that FR-I has a size of 1.5 kb and exists in variants which differ in the organization of two subfragments. Remarkably, the corresponding subfragments of either FR-I element were identical on the nucleotide sequence level. Although FR-I lacks terminal inverted repeats, the presence of terminal direct repeats and its occurrence in multiple copies suggest that FR-I represents a new type of archaeal insertion sequences. A second element, termed FR-II, is part of both plasmids pFV1 and pFZ1, and the chromosome of *M.thermoformicicum* THF, CSM3 and HN4. Sequence analysis of the two plasmid- and one chromosome-derived FR-II elements showed that they are highly similar and may code for a protein with yet unknown function. In contrast to FR-I, FR-II is present in a single chromosomal copy and does not contain terminal repeats. Its presence in plasmid- and chromosomal DNA suggests, however, that FR-II is mobile or has been mobilized.

Each plasmid contains an accessory element encoding components of a type II R/M system: the GGCC-recognizing system MthTI carried by pFV1 from strain THF (Chapter 7) and the CTAG-recognizing systems MthZI and MthFI located on pFZ1 and pFZ2 from strain Z-245 and FTF, respectively (Chapter 8). These findings demonstrated for the first time plasmid-encoded enzymatic activities for methanogens. The R/M systems MthTI and MthZI have been characterized in detail by their cloning and expression in Escherichia coli. Strikingly, both R/M modules are located within the same plasmid backbone region suggesting that this part of the plasmids has undergone substantial genomic rearrangements: either deletion or insertion of a single R/M module from an ancestral plasmid that contained both or none of the R/M cassettes. The presence of R/M cassettes would support the concept of a modular evolution, i.e., the mobilization of functional units within the same or between different replicons. Characterization of methanogenic R/M systems with the same specificity as the plasmid-located MthTI and MthZI systems may provide insight in the relationships of archaeal R/M systems and possible mechanisms of dissemination of R/M modules.

Supporting evidence for a modular evolution is provided by the similarity between the two GGCC-recognizing R/M systems MthTI from M.thermoformicicum THF and NgoPII from Neisseria gonorrhoeae (Chapter 7). In contrast to other R/M systems with GGCC specificity,

MthTI and NgoPII comprise endonuclease- and methyltransferase genes which both were similar on the nucleotide and the deduced amino acid sequence level and exhibit an identical organization (Figure 1). These findings suggest that the MthTI and the NgoPII systems are homologous and have been disseminated via horizontal gene transfer. If so, gene transmission would have occurred between members of the evolutionary different domains Archaea and Bacteria.

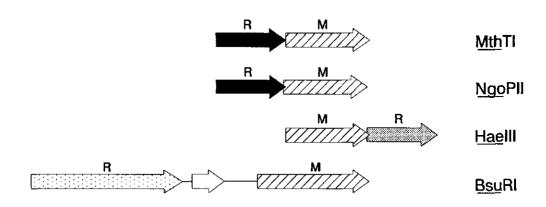


Figure 1. Gene organization of GGCC-recognizing restriction-modification systems. Homologous endonuclease (R) and methyltransferase (M) genes are indicated by similar shading.

An interesting property of the MthTI system is the fact that it is present in a thermophilic organism. In contrast, all other known GGCC-recognizing, or, more general, m5C-producing R/M systems, have been isolated from mesophilic organisms. The absence of such R/M systems in thermophiles has been attributed to an accelerated deamination rate of m<sup>5</sup>C (m<sup>5</sup>C - T) at high temperatures generating G-T mismatches in double-stranded DNA which, if not corrected, would result in point mutations (1) (Figure 2). The thermophilic M.thermoformicicum THF apparently contains a mechanism which either avoids deamination of m<sup>5</sup>C or is capable of G-T mismatch correction. The latter possibility seems to be realized in strain THF since the pFV1-located ORF10 has the capacity to code for a protein with significant similarity to E.coli DNA mismatch repair enzymes (Chapter 5; Figure 2). Similar to the organization of functionally related genes into operons, ORF10, mthTIM and mthTIR are located on the same pFV1 module (Figure 2) and may form a functional unit that specifies components of a restriction-modification-repair (RMR) system. Additionally, a putative fourth gene. ORF9, is located on the RMR module (Figure 2). Although no function could be assigned to the deduced ORF9 product, a participation in the activity of the RMR system would be plausible. Besides a possible common regulation, the observed gene clustering may also be necessary to ensure survival of a potential thermophilic recipient which acquires the RMR module via lateral gene transfer. However, if the recipient is a mesophilic organism, the DNA repair functions would probably be dispensable and may be lost after transfer. Assuming that a transfer of the entire RMR module has occurred from the thermophilic *M.thermoformicicum* THF to the mesophilic *N.gonorrhoeae*, this may explain why the similarity included the genes of the *Mth*TI and *Ngo*PII systems but did not extend beyond adjacent sequence regions.

The major function of R/M systems is proposed to be the protection of the resident DNA from contamination by for instance phage DNA (Figure 2). The same function may be supposed for the discussed R/M systems from *M.thermoformicicum*. However, one would expect that R/M systems which generate thermostable modification products such as m<sup>4</sup>C and m<sup>6</sup>A would be more advantageous for a thermophilic host than those that produce m<sup>5</sup>C, since deamination of the latter methylation product increases the chance on point mutations which have to be compensated by mismatch repair. Nevertheless, the m<sup>5</sup>C-generating *Mth*TI R/M system obviously proved to be successful under thermophilic conditions since it is maintained by *M.thermoformicicum* THF. A possible explanation for the presence of the *Mth*TI system in strain THF may be that the system provides another advantage to its host, in addition to restriction of incoming phage DNA by the *Mth*TI endonuclease. As discussed in Chapter 5, deamination of m<sup>5</sup>C may serve as additional protection mechanism against phages that contained m<sup>5</sup>C-methylated genomes since, in contrast to the host, these phages are not be able to correct mismatches.

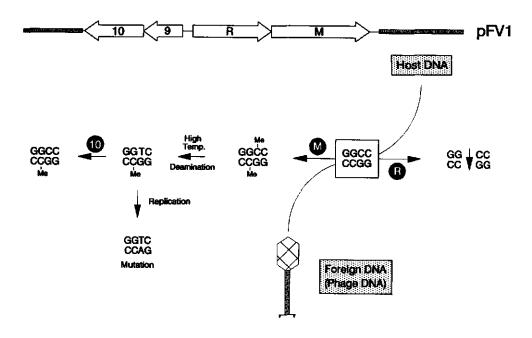


Figure 2. Schematic illustration of the proposed function of the restriction-modification-repair system harbored by plasmid pFV1 from *M.thermoformicicum* THF.

Analysis of the abundance of the tetranucleotide sequences GGCC and CTAG, the targets of the MthTI and MthZI R/M systems, in DNA of thermophilic Methanobacterium strains revealed some interesting results. The sequence data used for analysis comprised 48,4 kb of chromosomal and plasmid DNA, the majority of which were obtained from the EMBL and GenBank data bases (Table 2). The tetranucleotide GGCC was found 228 times within 48.4 kb, which statistically corresponds with 1 tetranucleotide per 212 bp. This value is almost equal to the expected random-frequency for a tetranucleotide which is 1 per 256 bp. In contrast, only 13 CTAG tetranucleotides were detected, corresponding with 1 per approximately 3700 bp. A similar low abundance of CTAG (1 per 2700 bp) has been reported for the E.coli genome (5). This finding clearly shows that the recognition sequence of the MthZI system, in contrast to that of the MthTI system, is rare in DNA from thermophilic Methanobacterium strains. However, a considerable different result was obtained from analysis of the plasmid DNA harbored by M. thermoformicicum. Compared to the values observed for the genomic DNA from thermophilic members of *Methanobacterium*, plasmid pFV1 exhibits a lower frequency of GGCC (1 site per 610 bp; 22 GGCC-sites per pFV1 genome) but shows a significantly higher abundance of CTAG (1 per 670 bp; 20 CTAG-sites per pFV1 genome)

Table 2. Distribution of GGCC- and CTAG-sites in DNA of thermophilic Methanobacterium strains

<b></b>	<b>0</b> !	0.7	Number	of tetranu	cleotides
Gene or element	Organism	Size (kb)	Expected <sup>b</sup>	Obse	erved
			-	GGCC	CTAG
sod	M. thermoautotrophicum sp.	1.4	5	5	0
purE	M.thermoautotrophicum sp.	1.4	5	4	0
rptTUVX	M.thermoautotrophicum Winter	7.5	29	50	1
hmtA	M.thermoautotrophicum ΔH	1.1	4	4	1
mvhGDGA	M.thermoautotrophicum ΔH	5.3	21	20	i
frhADGB	M.thermoautotrophicum ΔH	3.9	15	19	5
trpABCDGE	M.thermoautotrophicum Marburg	7.4	29	40	1
ileS	M.thermoautotrophicum Marburg	4.2	16	28	1
mcrBGA	M.thermoautotrophicum Marburg	6.2	24	15	3
pME2001°	M. thermoautotrophicum Marburg	4.4	17	18	0
FR-I	M.thermoformicicum CSM3	3.1	12	12	0
FR-II	M.thermoformicicum CSM3	2.7	11	13	0
	Total	48.4	189	228	13
pFV1°	M.thermoformicicum THF	13.5	53	22	20
pFZ1°	M.thermoformicicum Z-245	11.0	43	28	6

Comprising coding regions and flanking sequences.

b Random-frequency (on average 1 site per 256 bp).

<sup>°</sup> Complete nucleotide sequence

- (Table 2). While pFZ1 contains an comparable number of GGCC-sites (28 per plasmid genome with a frequency of 1 per 390 bp), the CTAG-frequency is substantially lower in pFZ1 from strain Z-245 (1 per approximately 1800 bp; 6 per pFZ1 genome) (Table 2). These results are interpreted as follows:
- (i) The low abundance of CTAG in the DNA of thermophilic Methanobacterium strains and E. coli suggests that a similar mechanism is responsible for this bias. It has recently been reported that the underrepresentation of several tetranucleotides, including CTAG, in the genome of E.coli may be the result of selection against target sequences of the vsr gene product (3), an enzyme involved in G-T to G-C mismatch correction (2). Usually, those target sequences of the Vsr endonuclease are generated by dearmination of m<sup>5</sup>C in the sequence C<sup>mc</sup>C(A/T)GG, the product of the dcm MTase. However, the vsr gene product displays a relative relaxed specificity since it also recognizes G-T mismatches in the sequence CT(A/T)G or T(A/T)GG where the underlined T is mismatched with G, and it does not require methylation of the unmutated strand (2). Consequently, T-G mismatches produced during recombination or DNA replication would, without determination which of both nucleotides is the incorrect one, sequence-specifically be corrected to C-G pairs. The tetranucleotide CTAG is one of the possible target sequences of the Vsr endonuclease and would be 'repaired' to CCAG, resulting in an elimination of CTAG-sites in time. A similar mechanism may be responsible for the low CTAG abundance in DNA of thermophilic members of Methanobacterium.
- (ii) Compared to the genomic DNA of thermophilic *Methanobacterium* strains, plasmid pFV1 of strain THF showed a five-fold increased number of CTAG tetranucleotides. This significant difference may indicate that selection against CTAG is absent in strain THF. Alternatively, pFV1 (and the related pFZ1 and pFZ2) does not originate from DNA of a thermophilic *Methanobacterium* strain. The relatively low GC content of pFV1 (41.8%) compared to that of strain THF (49.6%) (8) would support the latter possibility.
- (iii) Although pFZ1 of strain Z-245 is highly related to pFV1, the abundance of the tetranucleotide CTAG is clearly lower in pFZ1. Comparison of the nucleotide sequence of plasmid pFZ1 with the one from pFV1 showed that in particular CTAG-sites located within putative coding regions were absent in pFZ1. The lower frequency of CTAG-sites in pFZ1 correlates with the presence of the CTAG-recognizing *MthZI* system that is encoded by pFZ1. A possible explanation would be that the MTase M.*MthZI* provides only an incomplete protection against cleavage of the corresponding ENase which would result in selection against CTAG-sites. Another possibility may be that strain Z-245 contains a Vsrlike activity.
- (iv) The presence of the GGCC-recognizing *Mth*TI system encoded by pFV1 seems to correlate with the underrepresentation of GGCC-sites in the pFV1 genome. Comparison of the nucleotide sequences of pFV1 and pFZ1 revealed that 15 GGCC-sites present in pFZ1 were changed in pFV1. Remarkably, ten of those changed GGCC-sites in pFV1 displayed the sequence GGTC. The same base substitution would be generated by deamination of a single m<sup>5</sup>C nucleotides within the sequence GG<sup>mc</sup>CC followed by replication, i.e. without previous correction of the G-T mismatch. The observed preference for the replacement of GGCC by GGTC in pFV1 suggests that most of the substitutions have been generated by this mechanism. It therefore seems likely that strain THF has a limited G-T mismatch repair capacity. If so, strain THF should be forced to reduce the number of GGCC-sites available for modification by the m<sup>5</sup>C-producing MTase M.*Mth*TI in order to decrease the number of deamination events.

Most advances in physiological, biochemical and genetic analysis of *Methanobacterium* have been made on *M. thermoautotrophicum* strains  $\Delta H$  and Marburg (for reviews see: 6, 9). The present thesis focused on *M. thermoformicicum* and reported a genetic analysis of plasmids, phages and insertion sequences identified in this species. Since the well-studied methanogen *M. thermoautotrophicum*  $\Delta H$  turned out to be a non-formate utilizing relative of *M. thermoformicicum*, the here described mobile genetic elements may be instrumental in developing a cloning vector and a transformation system that would allow genetic engineering of strain  $\Delta H$ .

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## **Samenvatting**

De identificatie van de Archaea als een derde primaire levensvorm en hun adaptatie aan extreme omstandigheden hebben een aanzienlijke belangstelling gewekt voor de moleculaire biologie van deze organismen. De meeste vooruitgang in het onderzoek van archaeale mobiele genetische elementen, dat wil zeggen virussen, plasmiden en insertie elementen, is gemaakt binnen de groep van halofiele Archaea, maar er is weinig bekend over mobiele elementen in methanogenen (zie Hoofdstuk 1 voor een overzicht). Het doel van het in dit proefschrift beschreven onderzoek was om meer inzicht te verkrijgen in de moleculaire genetica van mobiele elementen in methanogenen. Als modelorganismen werd gekozen voor de thermofiele Methanobacterium soorten die tot de best bestudeerde methanogenen behoren.

Fylogenetische studies van M.thermoformicicum en M.thermoautotrophicum staan beschreven in Hoofdstuk 2. Door de vergelijking van twee variable 16S rRNA gebieden was het mogelijk te concluderen dat (i) M.thermoformicicum uit twee groepen van stammen bestaat, de zogenaamde Z-245-groep en de CB12-groep die waarschijnlijk tot verschillende species behoren. (ii) M. thermoautotrophicum AH nauw verwant is met de Z-245-groep, en (iii) M. thermoautotrophicum Marburg bij geen van de twee groepen behoort en waarschijnlijk een aparte species vormt. De uit de 16S rRNA analyse bepaalde verwantschap tussen stammen van M. thermoformicicum en M. thermoautotrophicum kwam overeen met resultaten van DNA-DNA hybridisatie studies (Touzel et al. [1992], Int. J. Syst. Bacteriol. 42, 408-411). Beide benaderingen zijn gebaseerd op genotypische eigenschappen die voor de bepaling van fylogenetische verwantschappen in het algemeen betrouwbaarder worden geacht dan fenotypische eigenschappen. De voorgestelde herindeling van de onderzochte thermofiele Methanobacterium stammen geeft daarom hun fylogenetische positie waarschijnlijk beter weer dan de indeling die tot nu toe gebruikt is. Een andere, fylogenetisch relevant aspect, gepresenteerd in Hoofdstuk 2, was de ontdekking dat de niet-formiaat gebruikers M. thermoautotrophicum AH en Marburg sequenties bevatten die overeenkomst vertoonden met de fdhA en fdhB genen van M, formicicum. De aanwezigheid van dergelijke sequenties in de stammen AH en Marburg suggereert dat M.thermoformicicum en M.thermogutotrophicum afkomstig zijn van een gemeenschappelijke, formiaat-gebruikende voorouder.

Hoofdstuk 3 beschrijft de karakterisatie van twee nieuwe archaeale virussen  $\Phi F1$  en  $\Phi F3$  die in staat zijn verschillende thermofiele *Methanobacterium* stammen te infecteren. Beide fagen verschillen wat betreft hun gastheerspecificiteit en de topologie van hun dubbelstrengs DNA chromosomen. Terwijl  $\Phi F1$  een breed gastheerbereik heeft en een lineair, ongeveer 85-kb genoom bezit, is  $\Phi F3$  specifiek voor *M.thermoformicicum* FF3 en bezit een circulair, ongeveer 36-kb genoom. Er bestaat geen overeenkomst tussen de genomen van  $\Phi F1$  en  $\Phi F3$ , noch tussen het genomische DNA van verschillende *Methanobacterium* stammen of van  $\psi M1$ , een faag van *M.thermoautotrophicum* Marburg.

De isolatie en karakterisatie van drie plasmiden, pFV1 (13,5 kb), pFZ1 (11,0 kb) en pFZ2 (11,0 kb), van de *M.thermoformicicum* stammen THF, Z-245 en FTF staat beschreven in Hoofdstuk 4. Door middel van hybridisatie met radioaktief gemarkeerd pFZ1 DNA bleek dat deze plasmiden een familie van nauw verwante elementen vormen. Terwijl pFZ1 en pFZ2 waarschijnlijk identiek zijn, wordt slechts een gedeeltelijke homologie gevonden tussen pFZ1 en pFV1. Daarnaast beschrijft dit hoofdstuk dat hybridisatie met het *fdh*A gen van *M.formicicum* gebruikt kan worden voor 'genetische vingerafdrukken' waardoor het mogelijk is om de species *M.thermoformicicum* in twee groepen te verdelen, de hierboven reeds

genoemde CB12-groep, met de stammen CB12 en SF-4, en de Z-245-groep met de plasmidebevattende stammen Z-245, FTF en THF en twee nieuwe isolaten FF1 en FF3.

De verwantschap tussen de plasmide DNA's werd bevestigd door de bepaling van de basenvolgorde van pFV1 (13513 bp) en pFZ1 (11014 bp) (Hoofdstuk 5). De vergelijking van deze sequenties liet zien dat de plasmiden pFV1 en pFZ1 in modules zijn georganiseerd: een ruggegraat struktuur, die geconserveerd is op DNA-sequentie niveau, en unieke sequenties met daarin opgenomen plasmide-specifieke elementen.

De organisatie van de *M.thermoformicicum* plasmiden is vergelijkbaar met die van bacteriële chromosomen waarin genetische herrangschikkingen optreden, in het bijzonder inserties en/of deleties, maar waarbij de basisstruktuur wordt bewaard. De grote overeenkomst in DNA volgorde en de vergelijkbare genetische organisatie doen vermoeden dat pFV1 en pFZ1 (en pFZ2) van een gemeenschappelijk voorouder-plasmide afkomstig zijn. In dit geval zouden de plasmiden voor vergelijkbare funkties coderen die van belang zijn voor vermenigvuldiging en handhaving. Deze zouden door de sequenties in de geconserveerde ruggegraatstruktuur gecodeerd kunnen worden. Zulke essentiële plasmidefunkties zouden twee grote palindroom-sequenties kunnen omvatten, alsmede een gen, dat mogelijk voor een NTP-bindend eiwit codeert. Al deze sequenties maken deel uit van de ruggegraatstruktuur die in de plasmiden wordt aangetroffen. In tegenstelling hiermee vertegenwoordigen de plasmide-specifieke sequenties juist additionele elementen die niet-essentiële plasmidefunkties zouden kunnen specificeren.

Beide plasmiden pFV1 en pFZ1 bevatten sequenties die overeenkomst vertonen met het chromosomale DNA van verschillende thermofiele methanogenen (Hoofdstuk 6). Een van deze sequenties, FR-I, is een additioneel element van pFV1 en heeft homologe tegenhangers in het chromosomale DNA van verschillende M.thermoformicicum stammen en M.thermoautotrophicum AH. Door vergelijking van de FR-I elementen afkomstig uit pFV1 en chromosomale DNA, kon afgeleid worden dat FR-I een lengte heeft van 1.5 kb en in varianten voorkomt die verschillen in de organisatie van twee subfragmenten. Opvallend was dat overeenkomende subfragmenten van verschillende FR-I elementen volledig identieke nucleotide sequenties bezaten. De FR-I elementen bezitten terminale, direkt herhaalde sequenties en zijn in meerdere kopieën aanwezig. Deze eigenschappen suggereren dat FR-I een nieuw type archaeaal insertie element vertegenwoordigt. Een tweede element, FR-II, maakt deel uit van beide plasmiden pFV1 en pFZ1 en werd aangetroffen in het chromosoom van M.thermoformicicum THF, CSM3 en HN4. Uit de DNA sequentie vergelijking van de FR-II elementen, waarvan er twee van plasmide DNA afkomstig waren en een uit het chromosoom, bleek dat de FR-II elementen sterk op elkaar leken en voor een eiwit met nog onbekende eigenschappen zouden kunnen coderen. In tegenstelling tot FR-I werd FR-II maar in een enkele chromosomale kopie gevonden en bezit het geen terminale herhaalde sequenties.

Elk plasmide bevat een additioneel element dat voor componenten van een type II restrictie-modificatie (R/M) systeem codeert: het *Mth*TI systeem van plasmide pFV1 uit stam THF met de herkenningssequentie GGCC en de CTAG-herkennenden R/M systemen *Mth*ZI en *Mth*FI die deel uitmaken van de plasmiden pFZ1 en pFZ2 van de stammen Z-245 en FTF. De gedetailleerde analyse van de systemen *Mth*TI en *Mth*ZI wordt beschreven in respectievelijk Hoofdstuk 7 en Hoofdstuk 8. Opmerkelijk is dat beide R/M modules in een vergelijkbare positie in de ruggegraatstruktuur van beide plasmiden gelokaliseerd zijn. Deze resultaten beschrijven voor het eerst een plasmide-gecodeerde functie in methanogenen.

Tenslotte wordt in Hoofdstuk 9 een samenvatting gegeven van de onderzoeksresultaten en worden enkele aanvullende gegevens besproken.

Complete nucleotide sequence of plasmid pFV1 from M.thermoformicicum THF (EMBL accession number X68366).

Numbering, open reading frames, insertions, inverted repeats (dashed arrows) and direct repeats (solid arrows) are according to Chapter 5.

1	KhOI  ELLVGTVRYNLIDNRVASGVLDCRGNGPGGSATKPEQVNH  CTCGAGAAGCACAGTGACGCGTAATTGAGTATATCGTTGCGAGCGCCTGCCT	120
121	L L N P F P G R L A L H Y N D H V L D I L S K G P V P I F E E V V K R P L R I H GAGAAGATTAGGGAAGGGCCTCGGGGGGAGATGATAATTGTCATGGAGGGGATCGATAGACTCTTTCCAGGGACGGGATAACTCCTCTACCACCTTTCTAGGAGCCGAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P M V	240
241	A N H T K G V L Q G Y N I H D A V R P D Y G R K L H P S D T E G R V A G R L K L TECATIGGGGGTCTTTCCACCAGATGACAGTGACGCTCCGGAGCTCGGGGGCTCTACAGCGCCCCCTTACAGCGCCCCCTACAGCGCCCCCGAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E	360
361	L D Q V V P N L H R K V V T D Q F V V N H W Q T R R E R G L T V P V G P I G K V GAGATCCTGAACTACAGGGTGAGGGGTTGAGGGTTTAACGACGGTGTCCCGGAGACGACGTTGTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D	480
481	E E A K R R I N R Y P L K L T N Y T L R Y D P H R S I L N L N L K D P T T D L L CTCCTCAGCTTTGCGGGGATATTGCGATAAGGCAGTTAAGGTTTAAGGTGTGTAAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTATCAGGCAG L L S F A A D I A I R Q L K G V V S E S D V R M A T D E V E V E F I R R S I E Q	600
601	Q P V I L L D E Q I G D H G G M P T G G S L Y I P L V V L H G L L L K P A V G K TTGAGGGCAATCAGAAGATCCTCCTGTATGCCGTCATGACCTCCCATGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGACCGAGGAGCAGTTTGGGGGCAACGCCCTT L R D N Q K I L L Y A V N T S H G G T P T E I Y R K Y N K M T E E Q F G G N A L	720
721	R L P P K G L E Q P F K F E V T K N F N L N D T P T T P P P N V P M ORF8  ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTACGGTCTTGTGAAATTGAGGTTGTCGGTAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S	840
841	(Insert element D in pFZ1) * ATTGACCCTGAACTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGACTACTTGGGGCAACTTTCTCTGGGTTTAAGTTGATTGA	960
961	TACTATTAACTTTTCTTTAATGGGGGTATCTAGGGCTTGTCCTGTAATCTTCCTGAGGTGCAGTGTCTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTGGTTGACCTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTGGTTGACCTTTTGGTTGACCTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTGGTTGACCTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTGGTTGACCTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTCAGAACAATTTTTCGTTCAATAAAATTGTTGGGTCTTTTGGTTGACCTTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTCAGAACAATTTTTTCAGAACAATTTTTCAGAACAATTTTTTTT	1080
1081	CTAGTTTGGTAATGTCCTATGGGTCGGCTAAGCGATTTCCGCCCTTTCGGGTCGCTCGC	1200
		1200
1201	TITAGGTAACCCATACCTCAACTTGTGATTTTGTGAATTTACCCCTTCACTCCGCCCCGACACTCTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT	1320
1321	- "	
1321 1441	TITAGGTAACCCATACCTCGACTTGTGATTTTGTGAATTTACCCCTTCACCCCCCCC	1320 1440
1321 1441 1561	TITAGGTAACCCAACCTCGTATTTGTGAATTTGCCCCTTCACCCCCCCACACCTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT	1320 1440 1560
1321 1441 1561 1681	TITAGGTAACCCAACCTCGACTTGTGATTTTGTGAATTTACCCCTTCACCCCCCCC	1320 1440 1560
1321 1441 1561 1681	TITAGGTAACCCATACCTGACTTGTGATTTTGTGAATTTACCCCTTCACCCCCCCGACACCTCTTATATAGACGCCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT	1320 1440 1560 1680

2161	AGTTCCTGTAGAAAAATTGACCTCTCCAAAAAGGATAGGAGGCGTTTTAAAATTCTTTCT	2280
2281	CTTGTGGACACCTAATCCYGCTAACAGTATAAATTYTTGGCATTATGAACCTCAGAGTGATGCCGACAAAGCACCTACAAGGTAACCTCAAATAGTTGTTTTAACTTGTTCTTTGGGGTG	2400
	L W T P N P A N S I N F W H Y E P Q S D A D K A P T R *	
2401	AGGGATTCACCCTCCCCAAAACCCCCCACCCGAAGGTCCCGGCGCTCGCT	2520
	IR6 4	
2521 2641	CCGGGTCGTTCGCTTCGCTCACTCTCGAATTTCCTAAAACAGCCGCTTTCGCTGCGTTACTCACATTTGGGCGGGAAAAACCAGTGAATGAGATCGGCGGGCG	2640 2760
	Element A (FR-I) ►	
2761 2881	AATATAAAGGTTTAATGACCTGTTTAATGCATTTTTCAGGTTTTTAGAATGTGAAATTATGGTGGCTGTCTTCGGTTGTAACCACCCTAGGAAATTTCTCTTTACAGGTTTCCGGCATCT TACAGGGATTAACCATATTTTGTTCTAAATCATTTTCAATATCAGTAATCAGAATATAAACAGATACTGAATTCAAAATATCCTTTTTTAAGTTGCTTAGCATTAAATCAAGGTATTCTTGAT	2880 3000
3001	TAGATTTTTCCATCAAACGCTTGATATCCTGATGTATAGCTTCTAATTTCATTCGGCATCATAGAATTCAGGATTATCCATTTTATTTA	3120
3121	ATAGTATTAAAGGTTTCTTTCTTGACCTTTTAAGTCATATTTGTGTATAAAACTGTACTTAGTACATTTTAATGACGGTTTAGTATATTTCTAATAAACAATAGTTATATTTGAAATT	3240
3241	AAAAACTTAATGGAGATGTGAAAATGGGAGTTAAAGAAGATATTCGTGGACAAATTATAGGAGCATTAGCAGGAGCCGATTTCCCAATAAATTCACCAGAAGAACTAATGGCAGCGCTTC	3350
3361	CAMACGETCCAGATACTACTTGTAAATCTGGAGATGTAGAATCTAAAAGCATCTGATGCTGGACAAGTACTTACT	3480
3481 3601	TAGTGAACAAAGCAGGATTATAAGCCAAAATCGACTTCCTACTTTTTCTTTTCTTTTCTTTTTTAAGGATAATTAAT	3600 3720
3721	AAGTCCTACTGCTTTCACTACAGATTAAATATTATAACAATCAAT	3840
3841	GATTATTTTTCAAATATTTTTTAAAATTACTGAGCATTATGAGTAGATTATATCCTTTTTCAGTAATCATATAATCTCCACGTTCATGACGCTGCAATATCAAGTCACTTTCAAGTAAAT	3960
3961	TTTTGTATGTGGAAAAGTAAATTACCACCACGAAGCCCTGTAAGTTCTGAAAGAGCAGTGAATGTCATGGTTTCAGAGGCCATAGATTTAAGAATTTGAAGTCTCTGTTTATTAGAAATA	4080
4081	GGTTCAAGAACACTCTTAACCATAATTTCTTCAGGAATAGAAGATATCTCAGTTTTATCCTCTTTATTATTGTCATATATTTGTCAGACCAATTAGATTTATTT	4200
4201	GAGTCTACTTCCTTAAAACAAATATCACATTTATCAAAAGGAGCACTTTTCCTTATTTCATCTAATTCCTCTCTTTTCTCTCTATAATTTCTTTGGAAACATGTTCCTGTTTTATAAGT	4320
4321	- Element A (FR-1)  TTAGAATTATTTTGTAGAAATCCGTTAAATTTTAATATGAAAAAATTAAATAATATTAATAAT	4440
4441	AACTTGAGGCAGAAAGTTATTGAAACCCTAGAAGAAGGGAAAAGTGTTGCGATTAAGTACCAGGATGTAAGGGATTACCTCGACCTGAAAACGGGTCATAGGGTTATATTCCTTGAACAC N L R Q K V I E T L E E G K S V A I K Y Q D V R D Y L D L K T G H R V I F L E H	4560
4561	GTTAACCCTGCAAAGGAGACAGCTGCTGAAATATTGGCTGACCTTGGCAACCTTGCAAAAAGCACTATATACAGCAAGTACACGAATGAGATTGTCAGGGACATCAAGAAGAGGTCG V N P A K E T A A E I L A D L G N Ł A K S T I Y S K Y T T N E I V R D I K K R S	4680
4681	AAGAACAGAAATGTCCTCCTAGTGTTCAATGACTTTCAGTTGCTTTCTAAGAACACTGCAAGGGTTCTTTTGGATCTCATGGAAGATGTCCAAGTTCTTTGTAGTATCCGGGGCAGACCC K N R N Y L L Y F N D F Q L L S K N T A R V L L D L M E D Y Q Y L C S I R G R P	4800
4801	CAGAAGGBTCAGGGGCGTTTGCTTAAGAGAATGACCATCCTAAGGBATAGGTCTGACGAGGTCACTGATATTAAGATACCCCTCATAGTCTTTGCGAGCTTTATAGCAATATTAACCTTT Q K G Q G R L L K R H T I L S D R S D E V T D I K I P L I V F A S F I A I L T F	4920
4921	GTTAAGGCGGGCTCGACCATCTATAACAGGAACCACTTCGACTTTTACCTGTTTTCTGCGGCAATTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGCATATCTGTGGGGAGGACTCTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGAGTATCTGTGGGGAGGACTCTTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGAGTAGGAGACTCTTTTTATGGATTTCTTAAGTTCAGGCAATTTTTTGTTGGAGTAGGAGACTCTTTTTATGGATTTCAGGCAATTTTTTGTTGGAGTAGGAGACTCTTTTTATGGATTTCAGGAGAATTTTTTTATGGATTTATGGAATTTTTTATGGATTTTATGGATTTATGGAGTAGAGAGACTCTTTTTATGGATTTCAGGAGAGACTCTTTTTATGGATTTCAGGAGAGACTCTTTTTAAGGATTTCAGGAGAATTTTTTATGGAATTTCAGGAGAATTTTTTATGGAATTTATGGAATTTTATGGAATTTTTAAGGATTTATGGAATTTTTAAGGATTATGAGAGAGAATTTTTT	5040
5041	V K A G S T I Y N R N H F D F Y L F S A A I F V G I S V G R T L L W I S *  GGTACCTCCTGTTTATATTCTGGGTCCTTATGGGCTTCGGCGGGCCTTATTACATTTTCTGGCTTTACGCCGTAGGTTATCAATAGGTCGGGGGTCGTGGTAATTTTGAAATGGTATAC  ORF4 M V Y	5160
5161	TCACGCCCTATTTTCTGTCTTTGTGSCGATATTCTTTGGTTATCTCTTGAACGCAGAGCTTTCACCATACTTTTTTATGTTGACAATTCTTTCGTCTGTAGTAGTGGACTTTGCAGAAAA S R P I F C L C G D I L N L S L E R R A F T I L F Y V D N S F V C S S G L C R K	5280
5281	GGCGGCGTTAACGAGCACAAAAGGCAACTTCACAATGTTTTCACCTTGATACCCTTTGTTCTCTTGTACTTTTTTTATGATGTGACCACAGGCGCCGCCATGTTGTCGGGCGTATCTTCC G G V N E H K R Q L H N V F T L I P F V L L Y F F Y D V Y Y G A A N L S G V S S	5400
5401	CATATTITGCTTGATTTTATGACGCCAACGGGCTGCCCCTTTTTTTACCCGATTTACAGGGGGCGTTATAGGGTCAATTGGAGGCATAAGGGTAGCGGTCCCAGGGAAAAAAGGGCGTTA H I L L D F M T P T G C P F F Y P I Y R G R Y R V M W R H K G S G P R E K R A L	5520
5521	ACAACTATAGGTATTCTTGCAGCGATTCTACTACTTGTCATCTATGCGCCGTCCCCATTTGCGCCGACTTCGGCAATTTCCCAGTGGAAGGGTTCTGGCAGCGGGGTCAATAACACGTCA T T I G I L A A I L L L V I Y A P S P F A P T S A I S Q W K G S G S G V N N T S	5640
5641	FR-II > AACAACGGGACGGACATAAATGTGAATTTTAACTTCAGGGGCAACGGTGACACCTGGATTCACCCTTACCCTAATGGCAGTATCTTCATTGACTGTGTGGGTGACAGTAACAGCAGGGTT N N G T D I N V N F N F R G N G D T W I H P Y P N G S I F I D C V G D S N S R V	5760
5761	TACAGGTATAGGGCTAGCAGCAGGGGAGGTCAAGGTAAGTACCTGAAATTGGATTCTAACACCACCGAAAACAAAACCACGAAGCAAAATGAGACGGGGGGATGACTCTGGCAAGGCGGA Y R Y R A S S R G G Q G K Y L K L D S N T T E N K T T K Q N E T G G *	5880
6001	GCCCTGCTTTTGAGAAGGTCTGCAGTTTTATAGAGAAGTCTGAGAGGTTCTGTACTGACAAGAAAATCTATACTCAGAAGGTTTACCTGGGACACTAGGACCGCCTGTAAGCTTGAGATTA TCAGCTATATCGAGTCAAAATCAAAAATCAAAAATGAACTTTCGAGGAGGCTATTAAGTTATTATAGACATATTGAATCTAAAAATGGACAACATAAAAAAAA	6000 6120 6240

6241	ACATTAGTGCTTGCAGCGCTCCTGACACTCTTTGTCCTTGCAGGTTCATCATCCGCGGGGTGTGGGGATTGAACTTGACAGAACATGAGTGAG	6360
6361	AATTCGACGATTAAAATCAAAGCCATAGTGAAGGCCTGGAACCTGGACGTTCAGAATGCCACTGCAAGGGTTCAACTTCCTGAGGGCCTCGTGGTGCAGGACTACTACATGAGCCAGGGA N S T I K I K A I V K A W N L D V Q N A T A R V Q L P E G L V V Q D Y Y M S Q G	6480
6481	TACTATGACCTCGAAACAGGTACCTGGGAGATTGGTGATATCCCAGCATATGAGGAGAGGTCCCTGACATTCATT	6600
6601	ACAGCGGACGGAGATGATAACAGTGCAAACAACAACGAGGTTAACCTTCAAGGTATTCGGTATATCAGACCTTGAGGTTAACGTCACAGGCAATAAAGAGACTGCAAGAATCGGCGAC T A D & D D N S A N N N A E L T F K V F G I S D L E V N V T G N K E T A R I 6 D	6720
6721	ACAGTGAGGATAACTGTTAAACTAAAACAGGGGCCCCCATGATGCGAATAATATCAAAATAGGCAACTTCCTCTCAGGGGGTCTTGTTGTGCAGAATTTCAGCTATGATGCGGCTAC T V R I T V K L K N R G P H D A N N I K I G N F L S G G L V V Q N F S Y D A G Y	6840
6841	TTTGATGACATCACCAGGGAGTGGATCTTTGAAACCCTTGCAGCAGGTGAGGGGCCAAATCAAAGCCATAGTGAAGGCCTGGAACCTGGACGTTCAGAATGCCACTGCAAGGGTTCAAC F D D 1 T R E W I F E T L A A G E E A K S K P *  ORF5b V K A W N L D V Q N A T A R V Q	6960
6961	TTCCTGAGGGCCTCGTGGTGCAGGACTACTACATGAGCCAGGGATACTATGACCTCGAAACAGGTACCTGGGAATTGGTGATATCCCAGCATATGAGGAGAGGTCCCTGACATTCATT	7080
7081	GCCTGCTGAACAGGACTGGCAGCGTTACTGTGAACGCCAATGTGACAGCGGAGGGAG	7200
7201	AGGTTAACGTCACAGGCAATAAAGAGACTGCAAGAATCGSCGACACAGTGAGGATAACTGTTAAACTTAAAACAGGGGCCCCCCATGATGCGAATAATATCAAAATAGGCAACTTCCTCT E V N V T G N K E T A R I G D T V R I I V K L K N R G P H D A N N I K I G N F L	7320
7321	CAGGGGGTCTTGTTGTGCAGAATTTCAGCTATGATGCGGGCTACTTTGATGACATCACCAGGGAGTGGATTGATAAACCCTTGCAGGAGGGAG	7440
7441	TGGTTAACAGGACGGGTGAGCTCTCAGACTATGTTTCAGTGCGTGAGGTCGATGAGGGCCGATGTGAATGTCTACAATAACATGGCCCATGCATCAGTGCTGTTAAGGGAACTGACCTAG L v n r t g e l s d y v s v r e v d e g d v n v y n n m a h a s v a v k g t d l	7560
	ACCTTGACCTCTCTGTGAGTAAACTGAGGGCATATCAGGGTGACGTGGTCAATGTGGTCTGCCGTGTCAGGAACAATGGTCCTGAGACCGCCCAGAATGCCAGGGTCAACCTCCAGCTAC D L D L S V S K L R A Y Q G D V V N V V C R V R N N G P E T A Q N A R V N L Q L	7680
	CGGGTAACCTGCAGGTCCAGCATGTGCAGCTGGACAGGGGCACCTACAGTAACGGTGTCTGGGTCATCGGTGACCTTGCAGACAATGAACAGCACTCCTCAATATAACCGCAAGGGTGA P G N L Q V Q H V Q L D R G T Y S N G V W V I G D L A D N E T A L L N I T A R V	7800
	TGTCAGCGGGTAACTTCACACTGAACGCCACTGCGGTTTCACCTGCAATCGACGACACCCCGTGAACAACGACGATAACACGACGATATCTGTAGCATAACAAAAAAAA	7920
	AGGTGAGGATAAAGAACACTCCGCAGTGACGATCAGGGTCCTCTTATATGTGACCGTCAATGATCATGGTAAAATAACCAGGAAGACCTACAACTTCTACCTGAAGAAGGGCCTCAGCA K Y R I K N N S A V T I R V L L Y V T V N D H G K I T R K T Y N F Y L K K G L S GGGACCTCAGCCTTGGATACTTCCAGCTGGGCACCACCGCACCTCTTCAAGCAGTACAACACCAACTACAAGTCCAGGTCAAGGACAGTATCCTATGAGAACACCTACAATGCCACCAGCG	8040 8160
	R D L S L G Y F Q L G T T A L F K Q Y T Y N T N Y R S R T V S Y E N T Y R A T S  TCATAACCCAGAGGGTCAACGTGTCTGGGGTCAAAGGAAGG	8280
	V I T Q R V N V S G V K G R Q K A P V V R I A T L L D E N G T S L Q *  ITHIAATTITITTAAGGTGTGGAATTGGTAGGAAGGAAACTCTCCAAGCAAATCTATGAGGCGATAGTTGTGATGAGGCAGAATGAGGGAAGGAGGTCTCCCAGCATGGCTT	8406
	ORF6 MRQIAEMRKEVSQHGF TGATGTCAGGATGATGGAAGTCCCTGGCATGAAGGTTGCTATCGCAGGTGATGGGGAAGTCAACTACAGTTTACTCCCCTTTAGGGACAAGTTTAAACTAAAAAGCGAGATGT	8520
8521	D V R M M E V P G M K V A I A G D G E V N Y L F M L L P F R D K F K L K K R D V  CTGGTTGTTCAAAAAACTTTCCTATAAATTCAAGGCAAGACCTTTCCTAGTAACTTTTGACAGATGTTATCTTTCTACCCACTACACGCCCTTGAAGAAGGTGGCGAACACTTTGAACT	8640
	W L F K K L S Y K F K A R P F L V T F D K M L S F Y P L H A L E E G G E H F E L  • FR-11	-314
8641	CGATATAAGGAATTCAAGGGGCTGATGTTTCTTTTGATACCATTGTGTCAGGCAGCAGTGCAACGGCTTGTTGTGTAGCCACCAAATGCCACAGCAGGTAACCCTAGCGGGTGTTT  D I R N S R 6 L M F S F D T I V S E Q L Q Q R L V V *	8760
8761	CCCTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	8880
8881	ATTGTGTTAAATTTGGTTTTTTGGGATTTCAGCACACTATTCTTTATGCAACGCTATAACGAAGGAATTGAAACCTTACGTCTTTATTTGGGTTTGCGCTTTGGGTTTGCCCCAACCCTAT  4 Element B	9000
	CTGGTCTCAGGGGTAATGAAAGTACTGCCAGGGTCACCATAGGGACTGTAACCTATCCACTAATCCACTAATATAATGTTAATACGATAATGTAATCTACAGTAGAATATTATAATCTGAAAGTATTAAAAAAGTATTAAAAAAGTATTAAAAAAAGTATTAAAAAA	9120 9240

9241	GRAGGAATACACTACCACCCAGTACGTCATCAACTTAAGGAAGG	9360
9361	TAGACATGAAGAAGGACCATGAAGCCAATCTTAAAGAAGAAAGA	9480
9481	TGCTGGACAAAAAGGAAAGGGAAGTCAACCACCTTGAAAATGAGGTCAGAAGGCTGCAGAACATGGGTCTATTTGAGATAATCCTAAACAAAC	9600
	T S C K E Y Y S C L K S N G C K E C K P K R P A C I I A AAGTTGAAGAGGGGGTTAAATAGACCCCAAGCCCTCAAGTACTACACTTCTCATAGTAGCTACAGAGTTTGCTCATCCACACTTTCTCACACTTTCTTGGGGCACATATGATTG L V E E G V K *	9720
9721	S F D M L G L M F D R C K G G P V L T E A L E W L A K H M Y M L N E Y S G G F Y CGGAAAGTCCATTAAACCAAGGTTAAAGTCCCTGCACTTTCCGCCAGGTCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCCAAAGTCCCCCAAAGTCCCCCCCAAAGTCCCCCCCAAAGTCCCCCCCC	9840
9841	R N I V R V F N A D V M A A K K G F A L C M V A A C T Y K G V G P L D L I A K R ACCTGTTANTAACTCTCACAAAATTTGCATCGACCATAGCGGCTTFTTTGCCAAATGCCAAACACTAACTGCAGCACAAGTGTATTTGCCAACTCCTGGTAGATCTAAAATTGCCTTCC	9960
9961	N R P V R G G Y D N I V V R A L E K L Q E A R Q N S L G I E K I D K A I E S K P TATTICGGGGCACTCTGCCCCCATAATCATTTATGACGACCCTTGCCAGTTCTTTTAGCTGTTCTGGCTTAGAGAGTCCGATTTCTTTATGTCTTTGGCGATTTCTGATTTTG	10080
10081	T K L I D E F C K Y K V F F K D Y I K K V H G A T T R R L L I E T I L I V Y P D GCGTTTTTAATATATCCTCAAAGCACTTGTACTTAACAAAAACTTGTCATATATCTTTTTAACATGCCCCGCAGTTGTCCTGCGAAGTAGGATTTCCGTTATTAAAATTACATAGGGGT	10200
10201	R T H R W P F D R R D T N W F T L I T S V F V K R K K N S A D D L ORFIO  + G I L D L G V H  CCCTCGTATGCCTCCAAGGAAAGTCGCGCCTATCTGTATTCCAAAACGTAAGTATGGTGCTAACGAAGACTTTCCTTTTTTTATTAGTAGCATCATCCAATTAAATCCAGCCCCACATGT	10320
10321	K L F L K K K A G L E K S V R N Y C D E L L D F L R V E G R W L N E V T N L G I TITAAAAATAATTTETTTTTAGCCCCTCAATTCCTTAGAAACCCTATTAGCAATCTTCTAATAAATCAAATAACTTCACCCCCCCC	10440
10441	A D V V D R L V T L S V F L D G L F S Y P G Y I E E P F M D L P S V S Y G L A A GCATCAACAACATCCCTTAAAACAGTTAAAGGATACAAAAAGGTCCCTAAAAACTATCCCTCTGGAAACATATCCAACGGCGAAACAGAATAACCAAGTGCAGCG	10560
10561	A V K L R D V E E L S E S R L L E A L L F L I E P L Y D V C D E Y E G R Y Q S L GCAACTITAAGCCTATCAACTTCTCCAAACTTCTGGAACTTCTGCTGAAAGATAATATCTCAGGTAGGT	10680
10681 10801	D E E F L R C I N G A R R I K V V M ORF9  TCTTCTTCAAAGAGTCTACAAATATTCCCTGCCCGCCTAATTTTAACCACCATAGTTTTATTTTTTTT	10800
10921	TGAACCAGATGGGAGTTACATTAGAAGGTTTTCCTAAAAGATGCTTTCTGCAATACATTTGATATAGAAAACAAAGACCTTGTGTACAGTGAATACTTTTCTTACCTTGGAAATCAAAAATA M N Q M G V T L E V F L K D A F C N T F D I E N K D L V Y S E Y F S Y L G N Q N	11040
11041	ACCCCCCGACATGATCCTGAAGGGGGGGTGACGCAGTTGAAGTCAAGAAGATAAAAGATAAAAACTTCGATTCAACTTAACAGTTCATACCCCAAGTCAAAGCTCTTTGTTTCTGACA	11160
11161	GCAGAATAACAGAGGCTTGCAAGAACTGTGAAGATTGGGAGGTTAAAGACATAATATATGCCATAGGGACTATCCCAAACAGAGTCCTTAAGTTAATGTTTTTTGTTTATGGGGACTGTT S R I T E A C K N C E D W E V K D I I Y A I G T I P N R V L K L M F F V Y G D C	11280
11281	ACGUGGCAAGCCCTTCTATCTACCAGAGAATTGYTGAAGAAGTAAAGGGGGGGTCTACATAGTACTGCCCTAGAATTTAGTGAAACAAAC	11400
11401	TGGGAATTACAGACCTAAGGGTACGTGGTATGTGGATCATCAAACACCCCCATAAAAGTGTTTAAAAACATAATCCCCCCCAGAATCAATTAAAAAATAATAACTTTAATTTAATTGCCCTGA	11520
11521	TGAAAGCAGAGAAGTATAAACAATTTCCAAAAAAAGATAGGAAAAGAATTGAGGCAGAAGTAATATCGAAGTTACCGATGTAAAAATAAAAGATCCTGACAACCCTGCCAAACTATTAG M K A E K Y K Q F P K K D R K R I E A E D N I E Y T D V K I K D P D N P A K L L	11640
11641	ATAGCGTTCTTGTGAGGTATGAATATGAATATGACATAGGCTCATTTTTTTCGGGTGCTGGAGGTCTCGACTTAGGGTTTACAAAAGCAGGTTTTAATATTGTCTTTGCTAACGA D S V L V R Y D E I *  mthTIN	11760
11761	CAATTGGAAAGGGTGCTGGAAAAACTTTCGAAAAAAACCACGGAATAAAAAAAA	11880
11881	CCCATGCCAGAGCTGGAGCCTGGCAGGTTCAATGTGCGGGGCAGACGACCCCCGTGGTAAAACATTTTATGCATACGTGGATTTAGTCAAAGAAAAAGATCCCCTATTTTTCTTGGCAGA P C Q S W S L A G S N C G A D D P R G K T F Y A Y V D L V K E K D P L F F L A E	12000
2001	AAACGTGCCAGGGATAGTTTCAAGAACACACCCCCCTGAATTCAAAAGACTTGTAAACTCATTCAT	12120

12121	GCCACAAGACAGAAAAAGGGTCTTTATCGTCGGGTACCGTGAGGACTTAAACCTAAAACTTTGAGTTTCCTAAACCTTTAAACAGAAAGTGACCCTGAGGGACGCTATTGGTGACCTTCC PQDRKRYFIYGYREDLNLKFEFFPKPENKYTLRADCAGAAAGTGACCGCTATTGGTGACCTTCC	12240
12241	YGAACCCAAGCCCGCGCTTGAAAAAACAGGTCAAATGGGGAAAACTTGGAAGTGCCAAACCACGAATACATGACAGGGACATTTTCAAGCAGGTATATGTCAAGGAACAGGGTAAGGAG E P K P A L E K N R S N G E N L E V P N H E Y M T G T F S S R Y M S R N R V R S	12360
12361	TTGGGATGAAGTTTCATTTACAATTCAAGCGGGGGGGCCCATGCCCCATGCCACCCCACAGGCTAATAAAATGATAAAGGTGGGACCTGACAAGTTCATATTGATCCAGAAAGTCCTAA W D E V S F T I Q A G G R H A P C H P Q A N K M I K V G P D K F I F D P E S P K	12480
12481	ACCCTACCGCAGGTTATCCGTCCGCGAATGCGCTAGGATACAAGGTTTTCCTGATGACTTTATATATA	12600
12601		12720
12721	AACAATACCTCTTTTAAGGTCCTCTTTTAAGGTCACAGAGAGTAAATTGCGAGTTGTAACCAGGAACAATACCTCTTTTAAGGTCACAGAGAGTAAATTGCGAGTTGTAACCAGGAACAA	12840
12841	TACCTCAAATTTTTTCATGAGTAATTTTTTTCATGAGCCAACTAGCCCACCACCACCACCACCACCACCACCACCACCACCAC	12960
12961	AAATCAAACCTTTCATATATAAAAAATTTTCAAGGTTTTTTACATGGCGAAATACAAGGAGTGTTGAACAGAAAGATTTGCCTGCTTTYGCTACAAGGTGTCCCTGTTACAATGTCTCTG	13080
13081	TTACAAGTGTTACAAGTAGAAATTCACTCTCTGTTTCCCAAGCAATGGGTTGTTTTTTGTTACAAGTAGAAATTCACTCTCTCT	13200
13201	* M Y F H P K S N Y L Q I A P L Q L P K L L S R GGTATTAATTCTTTCAATTAGAAATATATATATATATAGAAGTTATGAGTAGTGAGTGTTTGAGAAGA	13320
13321	SKEFVPIDEAREKKRVGQLLVSLFLHTSDALLVQPVDEVAGGGTACATCCTCGACGCCCCCCACGACACGACAGACAGA	13440
13441	W G V Q N Y P G W S R P L S D R R L I H D V F CCCACCCCACTGTATGTGAGGGCCCCAGGATGTGGGAGAGACTGTCACGAGAGAGA	13513

Complete nucleotide sequence of plasmid pFZ1 from M.thermoformicicum Z-245 (EMBL accession number X68367).

Numbering, open reading frames, insertions, inverted repeats (dashed arrows) and direct repeats (solid arrows) are according to Chapter 5.

| 1 CTCGAGAAGCACCACTGTACCCGTGATTGACGTACATCGTTGCGGACGGCACCGCCTACCAGGTCGCACCACTGTCCCAGGGCCCCCCGACGAGGTCTTGGGTTCCTGAACATR  L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I  L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I  121 GAGAAGATTAGGGAAAGGGCCCGGAGGGAAAGATTATACTGTACAGCGAGATCGATAGACCCTTTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGGGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGAGCCCCATTCTCCAGCGCCCCACTTCCAGCGCCCTTCCAGCGCCCCACTCTCCCAGCGAGCCCCTACAGGGTTCAGACCCTTTCAGCCCCCTACAGCCCCCCACCTGCGCCCTCCAGGGAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCACCTTCCAGCAGCCTTCCAGCAGCCTTCCAGCAGCCTTCCAGCAGCCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCGCCCCCCACCTTCCAGCGCCCCCCACCTTCAGGACCCCCACCTTCAGGACCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCCACCTTCCAGCCCCCCCACCTTCCAGCCCCCCCACCTTCCAGCGAGCCCCCCACCTTCCAGCGAGCCCCCACCTTCCAGCCCCCCACCTTCCAGCCCCCCACCTTCCAGCGAGCCCCCACCTTCCAGCGAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCCACCTTCCAGCGAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCGAGCCCCACCTTCCAGCGAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCTTCCAGCCCCCACCCCCCACCGCCCCACCTTCCAGCGAGCCCCTTCCAGCGAGCCCCTTCCAGCGAGCCCCTTCCAGCGAGCCCCTCACTTCTCCAGCCCCACCTTCCCACCACCCCCACCTTCCCACCTCCACCTTCCAGCCCCACCTCCACCTTCCAGCCCACTTCCACCACCTCCACCTTCCACCCCCACCTTCCACCA  | TACATCETTGCGGACGGCCTACCAGGTCGCAACGTCCATTGCCAGGGCCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  H D D Y H V L D I L G K G P V P I L E E V V K G P L R I H BATEATCATCGTATGGAGGAGATCGATAAGACCCTTTCCAGGGACGGGGATAGACTCCTTTCCAGGGAGCCGAATGTG  M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  H V H D A V R T R Y G R K L N P P D T E G R V A G R L K L CATEGAACTGATCGGCACTCGGGTGTTAATICCTCTTTAAGCCAAGGAGCACTTCAGAGGACCCCCCCCCAGACTTGAG  M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V TACACGACGGTGTCCTGGGAAGACGATGTTGCCACTTGCCACCTTGAC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I H P H R S I L N L N L K D P T T N L L GCACCTTAAGGGTTTGTCCAGCATCGTGAGGATGCACTCACACGACGACTCATGAGGTTTTTCAGCCACTCCCCAGGGGTTAACCTCTCAGCACTCCCCAGGGGTTCTCCAAGGTTTGTCACACTTGAGCACTCCCCAGGGGTTAACCTCTGAACTCCCAGGGGGGATCCCCCCACCACTTGAGATGATGAGGTTGAGGTTGAGGTTTATCAGGCATTTTAACCACTCTTGAC  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D H G G L P T G G S L Y I P L V V L H G L L K P A V G E CGTCATGACCTCCCAGGGGGGTACCCCCCCCTTGAGATATATAGGAAGGTACAACAAGATGGCGGAGGAGGAGACGATTTTTCCTCTCT  V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  K F E I A K D L N L N D A P A T P P P N V R M ORF8*  ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTTTCCTGGGATTTTTCCGGCAGGGGGCCGTTGGGAGGGGGGTTAACTGCCTTATTTTTTCCTTCTTCTCTCT  L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  CACCCCCCACTTTTTCCCTTGAGGGCAACTTTCTCTTGGATTTTTTGCCTTAAGGATGCCCCCATTTTTTTT  | LEKNTSDAVIEYIVA DGTAYQVATSIARAPRRGLGFLNIV  LLNPFPGRLSLHDDYNVLDILGKGPAVGGGGGAAAGATGATAGACCTTTCAGGGAAGGGGGAAAGATGATAGACCCTTTCAGGGAAGGGGCCGAATGTG  EKIRERASEGKNIIVNDEIDKTLSTTTCAAGGAGGAAAGATGATAGGACCGAGATGAGACCCTTTCAGGGAAGGGGAAAGATGATAGGACCGATGTG  EKIRERASEGKNIIVNDEIDKTLSRDGGAAAGAGGGGAAAGATGATAGAACCCTTTCAGGGAAGGGGAAAGACCCCTTTCAAGGGACCGAATGTG  EKIRERASEGKNIIVNDEIDKTLSRDGGAAAGAGGAGATGAATAGAACCTTTTCAGGGAAGGAGGAGAAGATTCCCCTTACAACCCCCCCC  | 1 CICCAGAAGCACCACTGACCACTTAGATCATTGGTACATGTTGGGSACGCCCACCAGGTCACCAGGTCATTGCCAGGCCCCCGACCAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLEEVEN CHARACTTTCAGGTCCTGAACATTGTGGTACATTGTGGTACATTGTGTCAGATTGTGTCAGATTGTGTCAGATTGTGTCAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGTGTAGATTGAGGAAGATTGAGGAACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGTAGACACCAGGATTGAGATGAGAGATGACAGAGATAGAT  | 1 CICGRAAGGCACCAGTGACGCGTTACAGTGTTACATCGTTGCGAAGGCACTCTCACAGGTTCACAGTGCTACAGGCTCTGCACAGTCTTGACATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  121 GAGAMAGTTAGGGAAAGGCCTCGAGGGAAGATCATATGGCGAAGATCATAGACCCTTTCAGGAGGGGGATCAGTCTCTCTAGCACCTTTCAGGGAACGGAACCATGTGT E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGGCTATGGGGTCTGGGTGTTATAGTCCTAGGGAGGG   | 1
CICAGAAAGCACAGCAGCAGCATTIGAGTACATGTTIGGSAAGGCACCCTACAGGTGCAAAGCTCTTIGCAGGGCCCCCCAACGGGTCTGGACTATTIGG L E K H T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L M I V  L L N P F P G R L S L H D D V N V L D I L G K G P V P I L E E V V K G P P R I B Y  121 GAGACAGTAGGGCATGGCCCCGAAGGGATTAGTAGGCAGGATCATAGAGCCTTTCAGGGACGGGGATAGTCCCTTTACAACGTTTCAGGGAAGGATCAGTAGGGATCAGGATCATAGGGCATGGGAGGATCAGTCCCTTTACAACGTTTCAGGGAAGGATCAGGATCAGTAGGACCTTTAGAGGAAGAGATCAGGATCATTAGGGAAGGATCAGTTCAGAGAGATCAGTTCAGAGAGTTAGAGACCTTTCAGAGAGTTAGGGAAGAAGAACAAGAAGATCAGAACAACAAGATGGCAAGATCAGAGTTAGAGAACAAGATAGAACAACAAGATGAAGAACAAGAACAAGATTAGAACAACAACAAGATTAGGAACAACAAGAACAACAAGAACAACAAGAACAACAAGAACAAC  | 1 CICGRAAGECACCACTGACCCCTTACAGCTTCACACTCCTACCACGTCCCACCAGCTCTTGCAGCTCTGACACTTGTGTCTCTCACCACTTCACAGCTCTGACACTTGTGTCTCACCACTTCACACCTCTACACCTCTCACACCTTCACACCTCTACACCTCTCACACCTTCACACCTCTACACCTCACCTCTACA | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CICAGAAGCACACAGCAGCACTATIGAGTACATCETTICGSAAGGCACCCCCACCAGCTCAGCAGGCTCTSGACTCTGACACTTGTG L E K H T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L M I V  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N I V  121 GAGACACTAGGGCATGGCCCCGAGGGGAGGATTAGATGCCCTTTTCAGGCCGTTCTCAGGAGCCGAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  124 TGCATTGTAGGCTTTCCACAAGCTTAGGCGCATGGGGATCGATTGTGCTGCTTTATACCTCTGCACCCTTTCACCACCTTTCAGCACCCCCCACCTTGAG C I V G L S N K L T V M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCTGAATACAGGTTGAGATGCCTTTAACCACTGTTCCTGAAGAGCATTGTTGCCCCCTTAACAGGTTGAACCACCTTTAACCTTTCACCCCTTTAACCACCCCCCCACACCTTGAAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R N G D A C A C A C C L V G L S N K L T V M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  481 CTCCTCAGCTTCAGAGGTTGAGATACCCCTTTAACCACCGTTCCTGAACCACCTTTGAGGCTTCTGCAACCACCTTGTGTGCAGCTTGTGTGAGATGCCCCCCACCCCCACACCTTGAACCACCATAGGCCACTTAGGCCATTGTGTGCAGTTGTGTGTG   | 1 CICAGAAGCACACAGCAGCACTATIGAGTACATCETTICGSAAGGCACCCCCACCAGCTCAGCAGGCTCTSGACTCTGACACTTGTG L E K H T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L M I V  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N I V  121 GAGACACTAGGGCATGGCCCCGAGGGGAGGATTAGATGCCCTTTTCAGGCCGTTCTCAGGAGCCGAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  124 TGCATTGTAGGCTTTCCACAAGCTTAGGCGCATGGGGATCGATTGTGCTGCTTTATACCTCTGCACCCTTTCACCACCTTTCAGCACCCCCCACCTTGAG C I V G L S N K L T V M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCTGAATACAGGTTGAGATGCCTTTAACCACTGTTCCTGAAGAGCATTGTTGCCCCCTTAACAGGTTGAACCACCTTTAACCTTTCACCCCTTTAACCACCCCCCCACACCTTGAAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R N G D A C A C A C C L V G L S N K L T V M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  481 CTCCTCAGCTTCAGAGGTTGAGATACCCCTTTAACCACCGTTCCTGAACCACCTTTGAGGCTTCTGCAACCACCTTGTGTGCAGCTTGTGTGAGATGCCCCCCACCCCCACACCTTGAACCACCATAGGCCACTTAGGCCATTGTGTGCAGTTGTGTGTG   
   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTICACAMAGEACACCAGTEACACGATTEACTACTTETICGSACGECTACCAGGTECACACTTICACAGGTECCACAGGTECTISACTTCTGSACTTCTGACACTTTGTG LEKNTSDAVIEYIVADGEAAAGCAGTTACAGGTECACACGTECACAGGTECTACAGGTECACACGTCCCCCCCCCC  | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG  
  | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTICACAMAGEACACCAGTEACACGATTEACTACTTETICGSACGECTACCAGGTECACACTTICACAGGTECCACAGGTECTISACTTCTGSACTTCTGACACTTTGTG LEKNTSDAVIEYIVADGEAAAGCAGTTACAGGTECACACGTECACAGGTECTACAGGTECACACGTCCCCCCCCCC  
   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC  
  | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC   | 1 CTCAGAAGCACCACCAGTGACCATTTGAGTACATCETTGGGACGGCACCCCCCCACCAGGTCTTGACCATTGTGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R R G L G F L N I Y  121 GASAMAGTTAGGGAAAGCGCTTGCGAGGGAAGATGATGAGACCCTTTTCAGGGACGGGGGATTGTGCACCCTTTTCAGGGACGGGACGATGTGG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCTTTCCACAAGCTTAGGGCACTGGGACTGTGATATCCTCTTTAGCCACAGTTTGACCCCCTTAGAGCGCCCCCACACTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGAGTGCGTTTTACCGCTGTTTCAGACGACTTGAGCCCCCCCACACTTGAG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R R G D A Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCAGCGCTATATGCCACTTAGAGCGCTTAGAGCTGTTGTTGTGAGTTGTGTGTG   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC   
   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC   | 1 CICIGAGA ACCASTRACCOST CATTAGE TACTOST TECSAL GEOCACCOCCIACACAGE TECCAS COCCCCCCACACAGA GET TEGET TOCT MARCATTETE LE N N N N N N N N N N N N N N N N N N   | 1 CICCAGAMACACACACAGETACCCCCATTAGACTACTICGEACGGCACCCCCTACCAGGTCCCACACAGGTCCATTAGCCCCCCCC   | 1 CTICGAGAAGCACCACTAGAGCGGTGATTAGATAGTCSTTCCGGAGGGCACCCCCTACCAGGTCGCGACAGCTCCTGATGCCCCCCCC  | CICCAGAGACACACAGTAGCCGTCATTAGATCACTCEGGACGCCCCACCACACAGCCCCCCCCCC  
   | 1 CICCAGAMACACACACAGETACCCCCATTAGACTACTICGEACGGCACCCCCTACCAGGTCCCACACAGGTCCATTAGCCCCCCCC   | 1 CICIGAGA ACCASTRACCOST CATTAGE TACTOST TECSAL GEOCACCOCCIACACAGE TECCAS COCCCCCCACACAGA GET TEGET TOCT MARCATTETE LE N N N N N N N N N N N N N N N N N N   | 1 CTICACAMAGEACACCAGTEACACGATTEACTACTTETICGSACGECTACCAGGTECACACTTICACAGGTECCACAGGTECTISACTTCTGSACTTCTGACACTTTGTG LEKNTSDAVIEYIVADGEAAAGCAGTTACAGGTECACACGTECACAGGTECTACAGGTECACACGTCCCCCCCCCC   | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG   | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG   
  | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG  | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG  | 1 CTICAGAAGACCACCAGTEACGCGGTATTAGATACTTCTTGCGGACGCCTACCAGGTCECAACGTCCTATCAGGGCCCCCCCCGACGAGGTCTTGGACTTCTGTGTGCCCCCTCACACGCCTCTACACGCCCCACGAGGTCTTGACCACTCTTCACACCTTTCCAGGGCACGCCCCCCCC  | 1 CTICAGAAGACCACCAGTEACGCGGTATTAGATACTTCTTGCGGACGCCTACCAGGTCECAACGTCCTATCAGGGCCCCCCCCGACGAGGTCTTGGACTTCTGTGTGCCCCCTCACACGCCTCTACACGCCCCACGAGGTCTTGACCACTCTTCACACCTTTCCAGGGCACGCCCCCCCC  | 1 CTICAGACAGCACCAGTEACGCGGTATTAGATACTICTGCGACGGCTACCAGGTCGCACAGTCTTGCCACCAGGTCTTGGACCTTGGACATTGTG L E K M T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L M I Y  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  121 GAGAMACTTAGGGCATTGCGAGGGAAGAGATCATAGGACACCATAGGACCATAGAGCCTTTCCAGGGAGGG  | 1 CTCGAGAGGCAGGCGGGGTATGAGTACATGTTGCGGAGGCGCACCAGGTCCTACCAGGTCCCACAGGTCCTAGCAGGCCCCCGACGAGGTCTTGGAGTCCTGACACTTGTG LEKNTSDAVIEYIVADGTAYQVATGTTCAGGCCCCCCCGACGAGGTCTTGGAGGCTCTGACACTTGTGAGCATTGTG LLNPFPGRLSLHDDYNVLDDILGKRPPRRGCAGTCGGCGACGAGGATCAGTAGAGCCCTTTCCAGCCCTTTCCAGGGAGGCCAGGGGGGGG   
   | 1 CTCACAGAGGACCAGTGACCAGTGACATGATTGAGTACATGTTGCGAACGGCTCACCAGGTCCACAGGTCCATGCCAGGCCCCCCGACGAGGTCTTGAGCTTCTGAACATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  121 GARAMATTAGGGAAGGCCTCGAGGGGAAGAGTCATGTGAGGACTCAATAGACCCTTTCTCAGGGAGTCGATCTCTCTC  | 1 CTCACAGAGGACCAGTGACCAGTGACATGATTGAGTACATGTTGCGAACGGCTCACCAGGTCCACAGGTCCATGCCAGGCCCCCCGACGAGGTCTTGAGCTTCTGAACATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  121 GARAMATTAGGGAAGGCCTCGAGGGGAAGAGTCATGTGAGGACTCAATAGACCCTTTCTCAGGGAGTCGATCTCTCTC  | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG  | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG  | 1 CTICAGAAGACCACCAGTEACGCGGTATTAGATACTTCTTGCGGACGCCTACCAGGTCECAACGTCCTATCAGGGCCCCCCCCGACGAGGTCTTGGACTTCTGTGTGCCCCCTCACACGCCTCTACACGCCCCACGAGGTCTTGACCACTCTTCACACCTTTCCAGGGCACGCCCCCCCC  | CIVAGA, ACADE, CALCASTERACE COSTRATTRAGETA ATTOSTICES ALCOSCA CACCAGA CACAGA CACAGA CACCAGA CACAGA CACACAGA CACACACA | 121 CTGGAGAAGCACCAGTGAGGGGTTGAGATAGTTGGGGAGGGCACCAGGTCGAGAGGCTCTGAGAGTTGGGACACTTGGAGAGGTCTGAGACTTGGG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  121 GAGAGAGTAGGGAGGAGGGGTTGAGAGGAGTCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  | 1 CTGGAGAAGCACCAGTGAGCGCGTATGAGTAGATGTTGCGGAGGGCACCGCCTACCAGGTCGGACACTTGCCGGGCCCGGGGGCTTGGATCTTGGTTCTGACATTGTG L E K IT S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L M I Y  121 GAGGAGGTTGGGGAGGGGGGGGGGGGGGGGGGGGGGGG  
   | 1 CTCGGAGGCAGCCAGGCGGTGATTGAGTACATCSTTGCGGAGGGCGCCACCGCGTGCCAAGGTCTTGGGTTCTGGACATTGTG  LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGGFLCTGGACGTCTGGACATTGTG  LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGGFLCTGGACGTCTGAGCATTGTG  121 GAGAGAGTTAGGGGAAGGGCCTTGAGGGGAAGAGTATGATGGAGATGAGAAGAGTCTCTCAGGGAGGG  | 121 CTICAGAAGCACCAGTGATCAGTACATCSTTECGGACGGCCACCGCTCACAGGTCCAGGGCCCCCCCACAGGTCTTGGATCATTGTG  LEKNTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  212 GAGAACATAGGGAAAGGCCTGCGAGGGAAAGATTGATGGATG  | 121 CTCGAGGAACCACCAGTGACGCGTATAGATTACATTCETTGCGACGGCCACGCGCTACAGTCTCAGGCCCCCCACAGCACGTCTTGGATCATTGTG 120 LEKNTSDAVIEYIVADGTAYQVAISIAARAPRRGCLGFLTAGACCATTGTGACCATTGAGGACCAATTGTGACCATTGAGGACCAATTGTGACCACCTTTCAGGGACCGAATGTGACCACCTTTCAGGGACCGAATGTGACCACCTTTCAGGGACCGAATGTGACCACCTTTCAGGGACCGAATGTGACCACCTTTCAGGGACCGAATGTGACCACCTTTCAGGGACCAATGTGACCACCTTTCAGGGACCAATGTGACCACCTTTCAGGGACCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGGCCAATGTGACCACCTTTCAGGCCCCCCCAGCCTTTCAGACCACCTTTCAGGCCCCCCCAGCCTTTCAGACCACCTCTAGACCACCTCTAGACCACCTTTCAGACCACCTTTCAGACCACCTCTAGACCACCTCAGACTACACCACCTTTCAGACCACCTCTAGACCACCTCTAGACCACCTCTAGACCACCTTTCAGACCACCTTCAGACCACCTCTAGACCACCTTCAGACCACCTTCAGACCACCTTCAGACCACCTTTAGACCACCTTCAGACCACCTCTAGACCACCTCTAGACCACCTTCAGACCACCTTCAGACCACCTTCAGACCACCTCAGACTTACAGGCATTCAGACAACATACAACAACAACAACAACAACAACAACAACAACA   | 121 CTGGAGGAGCACCAGTGACCGGTGATTGAGTACATCETTGCGGACGGCCACGCCTACAGTGCGCCACCAGGTCCTTGAGTTCTTGACATTGTG  LEKHTSDAVIEYIVADGTAAYQVATSIARAPRRGLGFLVTGAGACTGAGTCTGACATTGTG  LLHPFPGRLSLHDDYHVLDILGKGPVPJLEEVVKGPLRTH  122 GAGAAGATTAGGGCATGGGAGGAAGATATATATCTTCAGGGACGGGATAGAACCCTTTCAGGGACGGGGATAGACCCTTCTCAGGGACGGGATAGACCCTTTCAGGGACGGGATAGGACCCTTCTCAGGGACGGGATAGACCCTTTCCAGGGACGGGATAGACCCTTCTCAGGGACGGGATAGGACCCTTTCAGGGACGGAATGGGATAGAACCCTTCTCAGGGACGGGATAGACCCTTCTCAGGGACGGGATAGGACCCTTCCAGGGCCCCCCCC   | 1 CTCGAGAAGCACACCAGTGACGCGGTGATTGAGTACATCETTGCGGACGGCACCCCCTACCAGGTCCACAGGTCCACAGTCCACCAGTGCCACCCCCCACCAGAGGTCTTGGGTTCCTGAACATTGTG  L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  121 GAGAAGATTAGGGAAAGGCCTCGGGAGGGAAAGATGATTCGTTATGACCAGAACACCTTTCCAGGAACCCCTTCCAGGAACCGATGTG  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGGAAAGACTTACGGTCACGAACTGATCGGCGACTGGGGGTTATATGCTCGTTTAAGCCAGGAGCACTTTCCCCCCCTTACCAGGCCCCCCACCTTGAG  C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  150 GAGATCCTGAACTACAGGGTTCAGATGACCCGCGAACACCAGTTGTGCCCGGCGCTCGGCGCCCCCCCC   
  | 1 CTCGGGGGGCCCCCGGTGGATTGGGTACTGGTGGGGCGCCCCGGCGCGCCCCGGGCCCCCGGGGCCCCCGGGG   | 1 CICGAGAAGCACACCAGTGACGGGGTATTGAGTACATGGTTGGGGCCACCGGCCACCAGGGCCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG  L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGANAGATTAGGGGAAAGGGCCTCGGAGGGAAGATGATTAGGACGAATCAATAAGACCCTTTCAGGGAAGGGCCCCCCTTCCAGGACGCATGTG  E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACCAAGCTTACGGTCATGGGCCATCGGGTGTTATATCCTCGTTTAGACGAAGCACTATTGGCCCCCTACACGCCCCCCCC    | 1 CICGAGAAGCACACCAGTGACGGGGTATTGAGTACATGGTTGGGGCCACCGGCCACCAGGGCCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG  L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGANAGATTAGGGGAAAGGGCCTCGGAGGGAAGATGATTAGGACGAATCAATAAGACCCTTTCAGGGAAGGGCCCCCCTTCCAGGACGCATGTG  E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACCAAGCTTACGGTCATGGGCCATCGGGTGTTATATCCTCGTTTAGACGAAGCACTATTGGCCCCCTACACGCCCCCCCC    | 1 CICGGGGAGCCCCGGGGTTTGAGGTACTICGTTGCGGACGGCCCCCCACCGGTCCCAAGGTCCCAAGGTCCCAAGGTCCCAAGGTCCCGACCGA   | 1 CICGGGGAGCCCCGGGGTTTGAGGTACTICGTTGCGGACGGCCCCCCACCGGTCCCAAGGTCCCAAGGTCCCAAGGTCCCAAGGTCCCGACCGA   | 1 CTCGGGGAACCCGTGATCGCGTGATCGCGACGCGCTACCGGCTACCAGGTGCAAGGTCCAGGTGCCACGCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  LLHPFPGRLSLHDDYHVLDILGKGPAYGAGGGGAAAGGTCCTTACCACCTTTCCAGGGAAGGAGCAATGTG EKIRERASEGKAAGGGCTCGGAGGGGAAAAGGACTATGAGGAGAGAGCATCACCACCTTTCCAGGGAAGGAGCAACCACCATTTCCAGGGAAGGAGCAACCACCATTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAAGCTCCCCCACCCTTTCCAGGGAGCAGAGCAAGCTCCCCCACCCTTTCCAGGGAGGAGCAAGCA  | 1 CICGAGAAGCACACCAGTGACTGAGTACATCGTTGCGAGCGGCACCGCCTACCAGGTGCGAAGGTCCATGGCAGGGCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  LLHPFPGRLSLHDDYHVLDILGKGFACGGGGAACGAGGGGAACGAGGAGCCTTTCCAGGGGAGGGGAAGGCCCTTCCAGGGGAGGGGAAGGCCCTTCCAGGGAAGGGAAGGCCCTTTCCAGGGAAGGAGCCGAGGGAAGGCCCTTTCCAGGGAAGGGCCGAGGGAAGGCCCTTCCAGGGAAGGAA   | 1 CICGAGAAGCACACCAGTGACTGAGTACATCGTTGCGAGCGGCACCGCCTACCAGGTGCGAAGGTCCATGGCAGGGCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  LLHPFPGRLSLHDDYHVLDILGKGFACGGGGAACGAGGGGAACGAGGAGCCTTTCCAGGGGAGGGGAAGGCCCTTCCAGGGGAGGGGAAGGCCCTTCCAGGGAAGGGAAGGCCCTTTCCAGGGAAGGAGCCGAGGGAAGGCCCTTTCCAGGGAAGGGCCGAGGGAAGGCCCTTCCAGGGAAGGAA  
  | 1 CICGAGAGCACACCAGTGACGCGTGATTGACTACATCTTGCGGACGGCCCCACCAGGTGCCAACGTCCAAGGTCCCAGGGGCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKNTSDAVIEYIVA DGTAYQVATSIARAPRRGLGFLNIV  LLNPFPGRLSLHDDYNULDILGKGFACGCGGGGACCGACCGTTCCAGGGGCGGGGACCACCCTTTCCAGGGGCGGGGACCACCCTTTCCAGGGGACCGAATGGGGACCGAATGCCGTTCCAGGGACCGAAGCCCCTTTCCAGGGACCGAATGGGGAACGCCCTTCCAGGGACCGAAGCCCCTTCCAGGGACCGAATGCCGCCGACCTTTCCAGGGACCGAATGCCGCCGACCTTGCAGGGACCGAATGCCGCCGACCTTGCAGGGACCGAATGCCGCCCGC   | 1 CICGAGAAGCACACCAGTGACTGAGTACATCGTTGCGAGCGGCACCGCCTACCAGGTGCGAAGGTCCATGGCAGGGCCCCCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  LLHPFPGRLSLHDDYHVLDILGKGFACGGGGAACGAGGGGAACGAGGAGCCTTTCCAGGGGAGGGGAAGGCCCTTCCAGGGGAGGGGAAGGCCCTTCCAGGGAAGGGAAGGCCCTTTCCAGGGAAGGAGCCGAGGGAAGGCCCTTTCCAGGGAAGGGCCGAGGGAAGGCCCTTCCAGGGAAGGAA   | 1 CTCGGGGAACCCGTGATCGCGTGATCGCGACGCGCTACCGGCTACCAGGTGCAAGGTCCAGGTGCCACGCGACGAGGTCTTGGGTTCCTGAACATTGTG LEKHTSDAVIEYIVADGTAYQVATSIARAPRRGLGFLNIV  LLHPFPGRLSLHDDYHVLDILGKGPAYGAGGGGAAAGGTCCTTACCACCTTTCCAGGGAAGGAGCAATGTG EKIRERASEGKAAGGGCTCGGAGGGGAAAAGGACTATGAGGAGAGAGCATCACCACCTTTCCAGGGAAGGAGCAACCACCATTTCCAGGGAAGGAGCAACCACCATTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAACCACCACCTTTCCAGGGAAGGAGCAAGCTCCCCCACCCTTTCCAGGGAGCAGAGCAAGCTCCCCCACCCTTTCCAGGGAGGAGCAAGCA  | 1 CTCGGGGAGCCCCGGGGTTTCAGGTACATCETTGCGGACGGCCCCCCACCGGTCGCAGGTCCTAGGCCCCCCGACCGA   | 1 CTCGGGAGGGCCCTGGGGGGTATTGGTACATGTTGGGGAGGTCACAGGTCCACAGGTCCACAGGTCCTGGAGGTCTTGGGGTCCTGGAGCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P L R I H  121 GAGAGGTTAGGGGAAGGCCTCGGAGGGGAAGATGTAGGGGGAGATCGATAGACCCTTTCCAGGGGAGGGGGGGG  | 1 CITCACAMAGCACCAGTEACCAGTEACATCATTECGAACGCCACCAGCTCACCAGGTCCTACCAGGTCCCACCAGGTCTTGACCATTGTG L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I V  L L N P F P G R L S L H D D Y H V L D I L G K G P V P I L E E V V K G P P R I N I V  240  121 GAGAMANTIAGGGAAAGGCCTTGCAGGGAAGAGTCATAGCAGGAATCAATAGACCCTTTCCAGGGAGGG  | CICCAGAGACACACAGTAGCCGTCATTAGATCACTCEGGACGCCCCACCACACAGCCCCCCCCCC   
  | CICCAGAGACACACAGTAGCCGTCATTAGATCACTCEGGACGCCCCACCACACAGCCCCCCCCCC  | CICCAGAGACACACAGTAGCCGTCATTAGATCACTCEGGACGCCCCACCACACAGCCCCCCCCCC  | 1 CTCMASAMECRACCAGETEACECEGISTATICATECATECTICECSAGGEGECAGGEGECAGGEGECTTGGGTTCCTAGGGTTCTCAGACATTGGT   220  L E K N T S D A V I E Y I V A D G T A Y Q V A T S I A R A P R R G L G F L N I Y  L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240  E K I R E R A S E G K N I I V N D E I D K T L S R D G D K L L Y N L S R E P N V  A N Y A K G V L K R D H V N D E I D K T L S R D G D K L L Y N L S R E P N V  241  1721  173  174  175  175  175  176  177  177  178  178  178  178  178  |
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LLMPFPBGRLSLHDDYHVLDILGKGPVPTILEEVVKGPPLRI  121 GAGAMAATTAGGGAAAAGGCCTCGGAGGGAAAGATTATCATATGAGGAGATCGATAAGACCCTTTCCAGGGAGAGCCGAATTEEKIRGAGGAAAGGCGCCCGAATTEEKIRGAGGAAAGGCGCTCTTCCAGGGAAAGGCCCTCTACCACCTTTCCAGGGAGCCCAATTEEKIRGAGGAAAGCCTTTCCAGGGAAAGGCCTCTTCCAGGGAGCCCAATTEEKIRGAGGAAAGCCTTTCCAGGGAACCCCCCACACACACACACA	H D D Y H V L D I L G K G P V P I L E E V V K G P L R I H BATAGATCATCATAGACCAGATCAGATCAGACCCCTTTCCAGGGACCGAATGTG M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L CATAGACCATGACCGCCACTCGGGGTTATATCCCTCTTATACCCAGGGACCCGACCTTGAG M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V TAACGACCGTTCTCTGCAAGACCATCTTGTCCCCCTTGTCCCCCCTTCAAGCCCCCCCC	L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240  241  241  242  243  244  245  246  247  248  248  249  249  249  240  240  241  241  241  241  241  242  242	LLNPFPGRLSLNDDYNVLDILGKGPVPILEEVKGPLRIN  121 GAGAAGATTAGGGAAAGGGCCTCGGAGGGAAAGATTACTATGACCAGATCGTAGGACCGTAGGACCGAGGGGAAAGAGCCCTTCCAGGGAAGGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAAGCCCTTCCAGGGAACCCAACCTTCCAGGGAACCCAACCTTCCAGGGAACCCAACCTTCCAGGGAACCCAACCCTCGACCCCCCAACCTTCGACCACCCCCCAACCTTCGACCACCCCCCAACCTTCGACCACCCCCCAACCTTCAGACGCCCCCCAACCTTCAGACGACCCCCCAACCTTCAGACGACCCCCCAACCTTCAGACGACCCCCCAACCTTCAGACGACCCCCCAACCTTCAGACGACCCCCCAACCTTCAGACGACCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCTTCACACGACCCCCCCAACCCCCAACCCCAACCCCCAACCCCAACCCC
G R L S L H D D Y N Y L D I L G K G P V P I L E E V Y K G P L R I N  121 GASAMANTAGGGAAAGGGCCCGGAGGGAAGATGATCATGATAGGACCCTTTCCAGGGACGGGATAGCTCCTCTACCACCTTTCCAGGGACGCGATGTG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N Y  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTACTGCGCCATCGGCGATCTGGGTGTTATACCTCTTTAGCCAAGGGAGCACAGGTTTCCCCCCTTTCAACGCCCCCACCTTGACG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480  480  481 CTCCTCAACCTCAACGCTTACAGGCTTTAACGCCTTTAACGACGCTCTCCTGCAGGACGTTGTGCCCCCCTTTCAACGCCCCCCACCTTGAC  481 CTCCTCAGCTTCCAGCGATATTCCCATAAGGCACCTTAACGGTTCTTGCAGAGACATCTTGTGCCACCTCGCCGCCTCCGGCCCAGCCTCAGGGACGCCACCTTTAACGCACCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCACCTTCAACGCTTCAACGCACCTTCAACGCTCCCTCC   | L L N P F P G R L S L H D D Y N Y L D I L G K G P V P I L E E V Y K G P L R I N  121 GASAMANTAGGGAAAGGGCCCGGAGGGAAGATGATCATGATAGGACCCTTTCCAGGGACGGGATAGCTCCTCTACCACCTTTCCAGGGACGCGATGTG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N Y  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTACTGCGCCATCGGCGATCTGGGTGTTATACCTCTTTAGCCAAGGGAGCACAGGTTTCCCCCCTTTCAACGCCCCCACCTTGACG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480  480  481 CTCCTCAACCTCAACGCTTACAGGCTTTAACGCCTTTAACGACGCTCTCCTGCAGGACGTTGTGCCCCCCTTTCAACGCCCCCCACCTTGAC  481 CTCCTCAGCTTCCAGCGATATTCCCATAAGGCACCTTAACGGTTCTTGCAGAGACATCTTGTGCCACCTCGCCGCCTCCGGCCCAGCCTCAGGGACGCCACCTTTAACGCACCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCACCTTCAACGCTTCAACGCACCTTCAACGCTCCCTCC   | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCCGAAGGACCACATGAGACCCTTTCCAGGGACGGGACGCCACAGGCCCACAGGCCCACAGGCCCCCC  | L L N P F P G R L S L H D D Y N Y L D I L G K G P V P I L E E V Y K G P L R I N  121 GASAMANTAGGGAAAGGGCCCGGAGGGAAGATGATCATGATAGGACCCTTTCCAGGGACGGGATAGCTCCTCTACCACCTTTCCAGGGACGCGATGTG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N Y  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTACTGCGCCATCGGCGATCTGGGTGTTATACCTCTTTAGCCAAGGGAGCACAGGTTTCCCCCCTTTCAACGCCCCCACCTTGACG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480  480  481 CTCCTCAACCTCAACGCTTACAGGCTTTAACGCCTTTAACGACGCTCTCCTGCAGGACGTTGTGCCCCCCTTTCAACGCCCCCCACCTTGAC  481 CTCCTCAGCTTCCAGCGATATTCCCATAAGGCACCTTAACGGTTCTTGCAGAGACATCTTGTGCCACCTCGCCGCCTCCGGCCCAGCCTCAGGGACGCCACCTTTAACGCACCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCACCTTCAACGCTTCAACGCACCTTCAACGCTCCCTCC   | L L N P F P G R L S L H D D Y N Y L D I L G K G P V P I L E E V Y K G P L R I N  121 GASAMANTAGGGAAAGGGCCCGGAGGGAAGATGATCATGATAGGACCCTTTCCAGGGACGGGATAGCTCCTCTACCACCTTTCCAGGGACGCGATGTG E K I R E R A S E G K N I I I V N D E I D K T L S R D G D K L L Y H L S R E P N Y  A H Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTACTGCGCCATCGGCGATCTGGGTGTTATACCTCTTTAGCCAAGGGAGCACAGGTTTCCCCCCTTTCAACGCCCCCACCTTGACG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480  480  481 CTCCTCAACCTCAACGCTTACAGGCTTTAACGCCTTTAACGACGCTCTCCTGCAGGACGTTGTGCCCCCCTTTCAACGCCCCCCACCTTGAC  481 CTCCTCAGCTTCCAGCGATATTCCCATAAGGCACCTTAACGGTTCTTGCAGAGACATCTTGTGCCACCTCGCCGCCTCCGGCCCAGCCTCAGGGACGCCACCTTTAACGCACCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCCACCTTCAACGCCTTCAACGCCTTCAACGCCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCTTCAACGCTTCAACGCACCTTCAACGCACCTTCAACGCTTCAACGCACCTTCAACGCTCCCTCC   
   | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCCGAAGGACCACATGAGACCCTTTCCAGGGACGGGACGCCACAGGCCCACAGGCCCACAGGCCCCCC  | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIM  121 GAGAMGATMAGGGAAAGGGCCCGGAGGAGAAAGATGATCATCATGAGACCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGGCCCGAAGGGCEKAGAGCCCCTTTCCAGGGAAAGGGCCCTCCCGAAGGGACCGAAGGCCCCTTCCAGGGAAAGGGCCCCCCAAGGATCCAAGACCCCTTTCCAGGGAAAGGCCCCCCAAGGATCAGAGCCCCCCCAAGAGCCCCCAAGCCCCCAAGCCCCCAAGCCTTCAAGGCCCCCCCAAGCCCCCCAACCCCCAAGCCTTCAAGGCCCCCCCAACCCCCCAACCCCCAACCCCCAACCCCCAACCCC   | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCCGAAGGACCACATGAGACCCTTTCCAGGGACGGGACGCCACAGGCCCACAGGCCCACAGGCCCCCC  | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIM  121 GAGAMGATMAGGGAAAGGGCCCGGAGGAGAAAGATGATCATCATGAGACCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGGCCCGAAGGGCEKAGAGCCCCTTTCCAGGGAAAGGGCCCTCCCGAAGGGACCGAAGGCCCCTTCCAGGGAAAGGGCCCCCCAAGGATCCAAGACCCCTTTCCAGGGAAAGGCCCCCCAAGGATCAGAGCCCCCCCAAGAGCCCCCAAGCCCCCAAGCCCCCAAGCCTTCAAGGCCCCCCCAAGCCCCCCAACCCCCAAGCCTTCAAGGCCCCCCCAACCCCCCAACCCCCAACCCCCAACCCCCAACCCC   | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCCGAAGGACCACATGAGACCCTTTCCAGGGACGGGACGCCACAGGCCCACAGGCCCACAGGCCCCCC   
  | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCCGAAGGACCACATGAGACCCTTTCCAGGGACGGGACGCCACAGGCCCACAGGCCCACAGGCCCCCC  | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCGGAAGATGATCATGAGACCCTTTCCAGGGACGGGATGAGACCCCTTTCCAGGGAAGGGCCGCAAGATG EKIRERASEGKMIIVNDET TO KTLSRDGCAAGATCACCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGACGGAAGATGACCCCTTTCCAGGGAAGACCCCAAGATGAGCCCCCAAGATGAGCCCCCAAGACCCCAAGCTTAGAGCCCTTCCAGAGCCTAGACCCCCAACCTTGAGGCCCCCCCAACCTTGAGGCCCCCCCAACCTTGAGCCCCCCCAACCTTGAGCCCCCCCAACCTTGAGCCCCCCAACCTTGAACGCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCAACCAA  | LLMPFPGRLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIM  121 GASAMSATTAGGGAAAGGGCCCGGAAGATGATCATGAGACCCTTTCCAGGGACGGGATGAGACCCCTTTCCAGGGAAGGGCCGCAAGATG EKIRERASEGKMIIVNDET TO KTLSRDGCAAGATCACCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGAAGACCCCTTTCCAGGGACGGAAGATGACCCCTTTCCAGGGAAGACCCCAAGATGAGCCCCCAAGATGAGCCCCCAAGACCCCAAGCTTAGAGCCCTTCCAGAGCCTAGACCCCCAACCTTGAGGCCCCCCCAACCTTGAGGCCCCCCCAACCTTGAGCCCCCCCAACCTTGAGCCCCCCCAACCTTGAGCCCCCCAACCTTGAACGCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCCAACCTTGAACGCCCCCAACCAA  | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   
   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC   | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC  
  | LLMPFPERLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIH  121 GAGAMGATTAGGGAAAGGGCCCCGGAGGGAAAGATGATCACGTAAGACCCTTTCCAGGGAACGGAACGGAACGGAACGAAC   | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAMGATTAGGGAAAGGGCCCGGAGGAAGATCATCATGAGACCCTTTCCAGGGAACGGAACCCATAGGCCCTTCCAGGGACCGAATGTG EKIRERASE KMIIVNDEIDKLLVNLSRDPVV  241 TGCATTGTAGGGAAAGGGCCCCCCCATGTGAGGACCGAATGTGAGACCCCTTTCCAGGGAACCGAATGTGAGCCCCCCAATGTGAGCCCCCCAACTGTGAGCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGAGCCCCCCAACTGTGAGCCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCC  | LLMPFPERLSLHDDYNVLDILGESVKGPLRIH  121 GAGAMACTAGGGAAAGGCCCCGGAGGAAAGATCACCATAGACCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCAAGAGCCCTTTCCAGGGAACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCAAGACCGATGAGACCGAATGTG ANYAKEVLKRDHVHDAVRTYSRDGCATGCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. NYAKEVLKRDHVHDAVRTYSRDGCCTTAGACCCCCCCACCTTGAG CIVGLSNKLTVHDNIG DSGVISSFKPRRISFRYSAPQLE  4. DQVVPNLHRKVVTDQFVISAGACGACTTGCCCCGCGCGTTGAGCACCCCCCACCTTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCTGAGCACCCCCACCCCCCCC  | LLMPFPERRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAAGATTAGGGAAAGGGCTCGGAGGAAAGATGATTACTGTTAATGGAGAGATCCATAAGACCCTTTCCAGGGAAAGGATCCATACCACCTTTCCAGGGAACGGATGTG EKIRERASEGKMIIVNDEIDKLSRDPV  241 TGCATTGTAGGGAAAGGGCTCGGAAGGATCATAGACCACTTGAGGATCCATAGACCCTTTCCAGGGAACCGAATGTG 242 TGCATTGTAGGCCTTTCAACAACCTTAGACGCTATGCGCATTGAGGATCCATTAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTGAGGAACCACTTGAGGATCCATAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTAAGCAACGATGCCCACTGAGGATCCATTGAGCAACCACAACACACAC  | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAMGATTAGGGAAAGGGCCCGGAGGAAGATCATCATGAGACCCTTTCCAGGGAACGGAACCCATAGGCCCTTCCAGGGACCGAATGTG EKIRERASE KMIIVNDEIDKLLVNLSRDPVV  241 TGCATTGTAGGGAAAGGGCCCCCCCATGTGAGGACCGAATGTGAGACCCCTTTCCAGGGAACCGAATGTGAGCCCCCCAATGTGAGCCCCCCAACTGTGAGCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGTGAGCCCCCCCAACTGAGCCCCCCAACTGTGAGCCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCAACTGAGCCCCCCCC   
  | LLMPFPERLSLHDDYNVLDILGKGPPVPILEEVVKGPLRIH  121 GAGAMGATTAGGGAAAGGGCCCCGGAGGGAAAGATGATCACGTAAGACCCTTTCCAGGGAACGGAACGGAACGGAACGAAC   | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIM  121 GAGAMGATMAGGGAAAGGGCCCGGAGGAGAAAGATGATCATCATGAGACCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGGCCCGAAGGGCEKAGAGCCCCTTTCCAGGGAAAGGGCCCTCCCGAAGGGACCGAAGGCCCCTTCCAGGGAAAGGGCCCCCCAAGGATCCAAGACCCCTTTCCAGGGAAAGGCCCCCCAAGGATCAGAGCCCCCCCAAGAGCCCCCAAGCCCCCAAGCCCCCAAGCCTTCAAGGCCCCCCCAAGCCCCCCAACCCCCAAGCCTTCAAGGCCCCCCCAACCCCCCAACCCCCAACCCCCAACCCCCAACCCC  | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC  | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   
   | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   | LLNPFPERRLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGCCCCGAGGGAAAGATGATCATCGTATAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGCCCCCCCC   | LLNPFPERRLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGCCCCGAGGGAAAGATGATCATCGTATAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGCCCCCCCC   | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240 GAGMAGATIAGSBAAAGGGCCTCGGAGGBAAAGTGATCATAGAGCCGAGATAGACCCTTTCCAGGGACCGAATGGGCCTCTACCAGGGACCCAATGGGGACCGAATGGE E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P Y G P I G K V  GAGANICCTGAACTACAGGTTGACGATGGGTTTAAGGCCAGTGTGTGT   | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240 GAGAAGATTAGGGBAAAGGGCCTCGGGGGGAAAGATGATTAGAGACGATAGAACCCTTTCCAGGGACGAGACCCATTGCAGGGACCCATTGC E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  360 C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V  480 GAGANCCTGAACTACAGGGTTGAGATGGGGTTGCTGGAAGAGATGTGTTGCCCGGGGCCTGGGGGCCCGGGGCTTAGAGGACGAGATGTATAGAGCAGTTACAGAGATGAGATGAGAGTGTTGAGAGAGA  | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240 GAGAMAGTTAGGBAAAGGGCCTCGAGGBAAAGTGATTAGACGAGATCGATAGAGCCCTTTCCAGGGACGGGGACCGATGGGGCCGGGGCCGAGGGGCCGAGGGGCCGAATGGG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  360 C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P Y G P I G K V  480 GAGATCCTGACTACAGGGTTCACAGGGGTTCAGGGTTTCTGCAGGAGGTTTTTTAGCCCAGGGGCCCTGGGGGCCTGAGGGTTACGGGGGCCTGGGGGCCTGGGGGCCCTGAGGGTTACGGGGGTTCAGGGGGTTCAGGGGGTTCAGGGGGGGTTCAGGGGGGGG  
  | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  240 GAGAMAGTTAGGBAAAGGGCCTCGAGGBAAAGTGATTAGACGAGATCGATAGAGCCCTTTCCAGGGACGGGGACCGATGGGGCCGGGGCCGAGGGGCCGAGGGGCCGAATGGG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  360 C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P Y G P I G K V  480 GAGATCCTGACTACAGGGTTCACAGGGGTTCAGGGTTTCTGCAGGAGGTTTTTTAGCCCAGGGGCCCTGGGGGCCTGAGGGTTACGGGGGCCTGGGGGCCTGGGGGCCCTGAGGGTTACGGGGGTTCAGGGGGTTCAGGGGGTTCAGGGGGGGTTCAGGGGGGGG   | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   | LLNPFPERRLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGCCCCGAGGGAAAGATGATCATCGTATAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGAAAGGCCCCCCCC   | LLMPFPERLSLHDDYNVLDILGKGPVPILEEVVKGPLRIM  240 GAGMAGNTMAGGGAMAGGGCCTGGGAGGAMAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA   | LLMPFPGRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMAGTTAGGGAAAGGGCCTCGGAGGGAAAGACTAGACCCTTTCCAGGGAGGG   | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V Y K G P L R I N  240 GASAMAGTTAGGGBAAAGGGCCTCGGGGGGAAGAGTTAGACCCTTTCCAGGGAAGGGGAACCGATTGGC E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAAGGACTCAGGGTCAAGACCGGAACCGAATTGTAGACCCCCCCC  | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  121
GAGAMAGATTAGGGGAAAGGGCCTTGGAGGGAAAGATTCATAGACCCTTTCCAGGGACGGGGATTAGCTCTCTACCACCTTTCCAGGGAACCGATTGG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TECATTGTAGGCCTTTCCAGCACCTTACGGTCATGACATGA   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATTAGGGAAGGGCCTTGGAGGGAAAGATTATTCATAGACCCTTTCAGGAGAGGGGATAGACTCTCTACCACCTTTCAGGGAAGCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAACTTACGGTCATGGGCACTGAGGGCATGATGTTTTATACCTCTTTTAGACCAAGAAGAGGATCAGTTTGCCCCCCACCTTAGGG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R R R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGACGGTTCTGGAGAACAGATGTTGTGCCGGGCCCTGGGGCCCTGGGGCCCTGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCTCGGGGCCCCCAGCGTAATGGGACGCCCTTAGCGCTTCTGCC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCCCGGCGCATATTGCGATAAGGGGTTTGTCAGTGGAGTTGTGATGTGAGGTTGAGTTGCAGTGAGTTTAGTGTAGAGGTTAGTTTTACAGGCTTTTTATAGGGGGTTGTCAGTGAGGTTGAGTGTGAGTTGAGGTTGAGTTTAGAGGTTAGGGTTAGTTTTTAGAGGCGTATTTTTAGAGGCTATTTTTAGAGGCTATTTTTAGAGGTTGTTTAGAGGTTGTTTTAGAGGTGAGTTTGAGGATGAGATTAGGGGATAGAGATCAACAAGAAGGTTTTACCAAGGGTTGTTGTAGAGGTGAGTTTGAGGGGGGGG   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E Y V K G P L R I H  121 GAGAMGATTAGGGAAAGGGCCTTCGAAGGGAAAGATTGATCGTAATGGACGAATAGACCTTTCCAGGGACGGGATAAGCTCTCTACCACCTTTCCAGGGAACCGAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  141 TGCATTGTAGGCCTTTCCGACTCATCGGTCATGGACATGATCGGCGATCTGGGGTTATATCCTCTGTTTAAGCAAGGACGATCATCTTCGCCCCCACCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  A81 CACCCTAACCTCAACGGTTCAACGTCTCTGCAACACCATGTTCGCCCAGTTGTGCGCCGGCCCTCGGGGCCTCGGGCCCTCCGGGCCCTCCT  | LLMPFPGRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAMAGNTRAGGGAAAAGGGGCTCCGGAGGGAAAAGTGCACCATTCGAGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGGCCTTTCCAGGGAAAGGACCGATTGT EKIRERASEGKNIIVNDDILVNDEIDKTLSRDGATTAGCCTCTCTTCCAGGGACGGGATAGCTCCTCTTCCAGGGAAAGCGATTGTCGCCCCCCCC  | L L N P F P 6 R L S L H D D Y N V L D I L 6 K 6 P V P I L E E V V K 6 P L R I H  121 GAGAAGATTAGGGAAAGGCCTCGGAGGGAAAGATGATCATGTGATGGACGAGATCGATAAGACCCTTTCCAGGGAGGG  | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V Y K G P L R I H  121 GARAGATITAGGAAAGGGCCTCGGAGGGAAAGATGATTGGACCGAATCGATAGGACCTTTCCAGGGACGGGGGATAAGCTCCTCTTCCAGGGACCGAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACTGCGGCATCGGGGTGTTATATACCTCATTTAGCCCAAGGACGATCAGTTTCGCCCCTTACAGCCCCCCCACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R
R E R G L T I P V G P I G K V  A B C C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  A B C C I C A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGCGGGATATTGCGATAAGGCAGCTTTAAGGGGTTGTCAGTGAGTG  | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  240  121 GARAMGA ITAGGGAAAGGGCCTCGGAGGGAAACATGATCATCGTATGGACGAGATCGATAGAGCCTTTCCAGGGAGGG   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I H  240  121 GARAMGA ITAGGGAAAGGGCCTCGGAGGGAAACATGATCATCGTATGGACGAGATCGATAGAGCCTTTCCAGGGAGGG   | LLNPFPERLSLHDDYNVLDILGKKGPVPILEEVVKGPLRIM  121 GAGAAGATTAGGGAAAGGGCCTTGGAGGGAAAGTGATTATGACGAGATCGATAGACCCTTTCCAGGGAGGG   | LLNPFPERLSLHDDYNVLDILGKKGPVPILEEVVKGPLRIM  121 GAGAAGATTAGGGAAAGGGCCTTGGAGGGAAAGTGATTATGACGAGATCGATAGACCCTTTCCAGGGAGGG   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAMGATITAGGGAMAGGGCCTCGAGGGAMAGTIGATCATTAGGACGAGATCGATAMGACCCTTTCCAGGGAGGGGATAMGCTCCTCTTCCAGGGAGGGCGATATGG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  141 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGGCATCGGGCTGTTATATCCTCGTTTAGGCCAGGGCATCAGTTTGGCCCCCCCC   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATITAGGGAAAGGGCCTCGGAGGGAAAGATGATTAGGACGAATCGATAGGACCTTTCCAGGGACGGGGATAAGCTCCTCTTCCAGGAAGGGCCAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGACGTCGGGGTGTTATATACCTCGTTTAGGCCAAGGACGATCAGTTTGCCCCTTACAGGCCCCCCACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  1256 GAGATCCTGAACTACAGGGTTAGAGTGGGGTTTAACGACGTGTCTGGAACAGAGTGTTGTGCCCCTTGAACTACAGGGTTTAACGAGTTCTCTGGAACTACAGGGTTTAACGAGGTTCTACGAGGTTCCTCGGAACAGAGTTCTGGGGACAGTTCTGGGGGACAGTTTAAGGGTTTAAGGGTTTAACGAGGTTTAACGAGGTTCAAGGTTCTGGAACTACGAGGTTCAAGGGTTTAAGGGTTCTTAAGGAGTTCTAGTGGAACTACGGGGCCCCCGAGTTTAAGGGTTTAAGGAGTTCTAGTGGAACTACGGGGCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGTTCAAGTGTGAACTACGGGGCCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGGTTCAAGTGTAAGGCAAGTTCAAGGGTTCAAGTGTAAGGTTCAATGTGAAGGTTCAAGTGTAAGGGAAGTTCAAGAGGTTTAAGGGGAACTCAAGAGATTCTCCTGGGGACAGCTTAAGGGGTTTGTCAAGTGTGTGT   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATITAGGGAAAGGGCCTCGGAGGGAAAGATGATTAGGACGAATCGATAGGACCTTTCCAGGGACGGGGATAAGCTCCTCTTCCAGGAAGGGCCAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGACGTCGGGGTGTTATATACCTCGTTTAGGCCAAGGACGATCAGTTTGCCCCTTACAGGCCCCCCACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  1256 GAGATCCTGAACTACAGGGTTAGAGTGGGGTTTAACGACGTGTCTGGAACAGAGTGTTGTGCCCCTTGAACTACAGGGTTTAACGAGTTCTCTGGAACTACAGGGTTTAACGAGGTTCTACGAGGTTCCTCGGAACAGAGTTCTGGGGACAGTTCTGGGGGACAGTTTAAGGGTTTAAGGGTTTAACGAGGTTTAACGAGGTTCAAGGTTCTGGAACTACGAGGTTCAAGGGTTTAAGGGTTCTTAAGGAGTTCTAGTGGAACTACGGGGCCCCCGAGTTTAAGGGTTTAAGGAGTTCTAGTGGAACTACGGGGCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGTTCAAGTGTGAACTACGGGGCCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGGTTCAAGTGTAAGGCAAGTTCAAGGGTTCAAGTGTAAGGTTCAATGTGAAGGTTCAAGTGTAAGGGAAGTTCAAGAGGTTTAAGGGGAACTCAAGAGATTCTCCTGGGGACAGCTTAAGGGGTTTGTCAAGTGTGTGT   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATTAGGGAAAGGGCCTCGGAGGGAAAGATGATTAGGACGAATCGATAGGACCCTTTCCAGGGACGGGGATAAGCTCCTCTTCCAGGACGACCCATTTCCAGGAAGGGCCAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGGGGGACTTGGGGGTGTTATATGCTCGTTTAGGCCAAGGACTCAGTTTGGCCCCCCCC  
  | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATITAGGGAAAGGGCCTCGGAGGGAAAGATGATTAGGACGAATCGATAGGACCTTTCCAGGGACGGGGATAAGCTCCTCTTCCAGGAAGGGCCAATGTG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  1241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGACGTCGGGGTGTTATATACCTCGTTTAGGCCAAGGACGATCAGTTTGCCCCTTACAGGCCCCCCACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  1256 GAGATCCTGAACTACAGGGTTAGAGTGGGGTTTAACGACGTGTCTGGAACAGAGTGTTGTGCCCCTTGAACTACAGGGTTTAACGAGTTCTCTGGAACTACAGGGTTTAACGAGGTTCTACGAGGTTCCTCGGAACAGAGTTCTGGGGACAGTTCTGGGGGACAGTTTAAGGGTTTAAGGGTTTAACGAGGTTTAACGAGGTTCAAGGTTCTGGAACTACGAGGTTCAAGGGTTTAAGGGTTCTTAAGGAGTTCTAGTGGAACTACGGGGCCCCCGAGTTTAAGGGTTTAAGGAGTTCTAGTGGAACTACGGGGCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGTTCAAGTGTGAACTACGGGGCCCAGCTGAAGGAGTTCAAGGGTTCAAGGGTTCAAGGGTTCAAGTGTAAGGCAAGTTCAAGGGTTCAAGTGTAAGGTTCAATGTGAAGGTTCAAGTGTAAGGGAAGTTCAAGAGGTTTAAGGGGAACTCAAGAGATTCTCCTGGGGACAGCTTAAGGGGTTTGTCAAGTGTGTGT   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAMGATITAGGGAMAGGGCCTCGAGGGAMAGTIGATCATTAGGACGAGATCGATAMGACCCTTTCCAGGGAGGGGATAMGCTCCTCTTCCAGGGAGGGCGATATGG E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  141 TGCATTGTAGGCCTTTCCAACAAGCTTAGGACATGGGCATCGGGCTGTTATATCCTCGTTTAGGCCAGGGCATCAGTTTGGCCCCCCCC   | L L N P F P G R L S L H D D Y N V L D I L G K G P V P I L E E V V K G P L R I M  121 GAGAMGA ITAGGGAAAGGGCCTCGAGGGAAACTGATCATCATAGGACGAGATCGATAGGACCTTTCCAGGGACGGGATAMGCTCCTCTACCACCTTTCCAGGAAAGGGCCTATTGGACGACGATCGAT   | L L N P F P G R L S L N D D Y N V L D I L G K G P V P I L E E V V K G P L R I N  121 GAGAAGATTAGGGAAAGGGCCTCGGAGGGAAAGATCATTAGACCCTTTCCAGGGACGGAGCCGATGGG  E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGCCTTTCCAACGACCTTAGGCTCAGGACGGAGTGGGTTAGATCCTCTTTAGACGACGGGCCCGCACCTTGAG  C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N H Q A R R E R G L T I P V G P I G K V  480  GAGATCCTGAACTACAGGGTTCCAATGCCTTTAACGCACGTTGCTGGAAAGAGATCTGTGCCCGGGCCCTGAGGGCCCTGAGGGTTCAAGGGACCCAAGCTTAAGGCACCTTAAAGGACGTCCTTGAAGCAAGTTCTCACCGGGCCCTGAGGGTTCAAGGGACACCAAGGATTTGAACGACGTTCTGCAAGAGATGCTTCTGTGCCGGGCCCTGAGGGCCCTGAGGGACACCAAGGATTTGAACGACGTTTCTGCAAGAGATTCTGAGGAGTTGAAGGACGACCAAGGATTTTGAACGAAGTTTGAAGAGATTCTGAAGAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGCAAGTTCTCAAGTTTGAGAGTTGAAGATTGAGAGTTGAAGATTTAAGAGATTTGAGAAGA   | LLNPFPERLSLNDDYNVLDILGKGPVPILEEVVKGPLRIN  121 GAGAMGATTAGGGAAAGGGCCCGGAGGGAAAGATGATCATGTAAGACCCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACGGAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCCC   | LLMPFPERRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAAGATTAGGGAAAGGGCTCGGAGGAAAGATGATTACTGTTAATGGAGAGATCCATAAGACCCTTTCCAGGGAAAGGATCCATACCACCTTTCCAGGGAACGGATGTG EKIRERASEGKMIIVNDEIDKLSRDPV  241 TGCATTGTAGGGAAAGGGCTCGGAAGGATCATAGACCACTTGAGGATCCATAGACCCTTTCCAGGGAACCGAATGTG 242 TGCATTGTAGGCCTTTCAACAACCTTAGACGCTATGCGCATTGAGGATCCATTAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTGAGGAACCACTTGAGGATCCATAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTAAGCAACGATGCCCACTGAGGATCCATTGAGCAACCACAACACACAC  | LLMPFPERRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121
GAGAAGATTAGGGAAAGGGCTCGGAGGAAAGATGATTACTGTTAATGGAGAGATCCATAAGACCCTTTCCAGGGAAAGGATCCATACCACCTTTCCAGGGAACGGATGTG EKIRERASEGKMIIVNDEIDKLSRDPV  241 TGCATTGTAGGGAAAGGGCTCGGAAGGATCATAGACCACTTGAGGATCCATAGACCCTTTCCAGGGAACCGAATGTG 242 TGCATTGTAGGCCTTTCAACAACCTTAGACGCTATGCGCATTGAGGATCCATTAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTGAGGAACCACTTGAGGATCCATAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTAAGCAACGATGCCCACTGAGGATCCATTGAGCAACCACAACACACAC  | LLMPFPERRLSLHDDYNVLDILGKGPVPILEEVVKGPLRIH  121 GAGAAGATTAGGGAAAGGGCTCGGAGGAAAGATGATTACTGTTAATGGAGAGATCCATAAGACCCTTTCCAGGGAAAGGATCCATACCACCTTTCCAGGGAACGGATGTG EKIRERASEGKMIIVNDEIDKLSRDPV  241 TGCATTGTAGGGAAAGGGCTCGGAAGGATCATAGACCACTTGAGGATCCATAGACCCTTTCCAGGGAACCGAATGTG 242 TGCATTGTAGGCCTTTCAACAACCTTAGACGCTATGCGCATTGAGGATCCATTAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTGAGGAACCACTTGAGGATCCATAGACCACTTGAACCACCCCCAACTTGAG CIVGLSNKLTVNDNIGSSTAAGCACCACTTAAGCAACGATGCCCACTGAGGATCCATTGAGCAACCACAACACACAC  | L L N P F P G R L S L H D D Y N Y L D I L G K G P Y P I L E E Y Y K G P L R I N 240  241  242  243  244  245  246  247  248  248  249  249  249  249  240  240  241  240  241  241  241  241   |
| 21 GAGANGATTAGGGAAAGGGCCTCGGAGGGAAAGATGATCATGGTAATGGACGAGATCGATAAGACCCTTTCCAGGGACGGGATAAGCTCCTCTACCACCTTTCCAGGGAGCCGAATGE E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGACATGGGCGACTGGGGTGTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCCCCGCACCTTC C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K  361 GAGATCCTGAACTACAGGGTTGAAGGAGGGTGTCCTGGGAGAGGATGTTGTGCCCCTTGCGGGCCCCGGGCCCTGCGGCCCAGCGTAATGGGGACCCCGGGTTTACAGCCCCTGGGAGAGCATGTTGCCCTTG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L  CTCCTCAGCTTCGCGGCGCGATATTGCGATAAGGCAGCTTTAAGGGTTTTCCAGTCAGCTCTGAGTTGGGCGCGCCTGCGGGCCCACGGGATAGGGTTGAGTTTTCAGGCGTTTATTTCAGCCTTAAGGATTACAGCAGTTGCCCTTGAGGATATAGGAAGTTACAACAAGATGCCCGATGAGGATGCCAGAGATACAACAAGATGCCCGATGAGGATGCCAGAGAACACCAGAAGATCCTCCTGTAGGCCGCTTAAGGCAGCTCCCCAGGGGGGGTAACCCCCACTGAGGATACAACAAGATGCCCGAGGAGAACACCAGAAGATCCTCCTGTAGGCCGCTCACGGGGGGGTACCCCCACTGAGGATACAACAAGATGCCCGAGGGGGAGAGCAGCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N QRF8  721 ACCCAGAGGACTTCCCAGCTCCTAGGGGAACTTGAACTCTATGGCCTTGCGAGACTTCTCTGGGGGGGG  | AT TEST OF FIRE VERSIBLE VERSI | 240 241 TREE RASE GRANDISTANCE TO THE CONTROL OF TH | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  TECATIGIAGGCCTTTCCAACAGGCTTACGGTCATGGATGATGGGGGGTTATATCCTTGGTTTATAGCTAGGTATGGTTTGGCCCCTTTACAGGGACGAGCCCCCCAGGGTTGAG  C C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAAGGACGGTGTCCTGGAAGAGGATTGCCCCTGAGGGGGGGG  | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATIGNAGCCTTCCACCAGCTTCCGCCAGCCCATGGG GGGGGGGGGG   | 240  241 GRAMAGATHAGGGAAAGGGCCTGGGAGGGAAAGGATCGATAGGACCCTTTCCAGGGAGGG  | 240  241 GRAMAGATHAGGGAAAGGGCCTGGGAGGGAAAGGATCGATAGGACCCTTTCCAGGGAGGG  
   | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TEGATIGIAGRACAGEGGCATAGEGGCATGEGGGGGGGGGGGGGGGGGGGG   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T T G R V A G R L K L  241 TEGATIGIAGECCTICACAGCITICAGECAGCITAGACTCGEGGTTAGACTCGTTTAGACCAGCAGGAGGTTGGGGCCCGCAGCTTGAGG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAGTTACAGGGTTTAGACGAGGTTCGGGGTTCTGGGAGAGGAGTTGTGGGGGGCCCGGGGCCTAATGGGGAGCCGGGGCCTTGAGG E I L N Y R V E M A F N D G V I E D D V V P L C A A L A A Q R M G D A R Y A L Q  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGGGGGATATGGGGATTAGGGGCGTTTAGGGGGGGTTGAGGTTGAGGGGGGGG  | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T T G R V A G R L K L  241 TEGATIGIAGECCTICACAGCITICAGECAGCITAGACTCGEGGTTAGACTCGTTTAGACCAGCAGGAGGTTGGGGCCCGCAGCTTGAGG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAGTTACAGGGTTTAGACGAGGTTCGGGGTTCTGGGAGAGGAGTTGTGGGGGGCCCGGGGCCTAATGGGGAGCCGGGGCCTTGAGG E I L N Y R V E M A F N D G V I E D D V V P L C A A L A A Q R M G D A R Y A L Q  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGGGGGATATGGGGATTAGGGGCGTTTAGGGGGGGTTGAGGTTGAGGGGGGGG  | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TEGATIGIAGRACAGEGGCATAGEGGCATGEGGGGGGGGGGGGGGGGGGGG   | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TEGRATIGNOGECTICCAGGAGGGGAATGGATCAGTAGGACCTTTCCAGGGAGGG  
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   | PAGAMAGN TRAGGGAAAGGGCCTCGSAGGGAAGGTCATTCATCGTANTGGACGGATCGATTCTCAGGGACGGGATAGCTCCTCTTCCAGGGAGCCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D B D K L L Y H L S R E P M V  A H Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACAAGCTTACGGCTCTGGGAGTTGTATATCCTCTTTAGCCAGAGGAGCCCTTTAGAGCCCCGCACCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGGATTGCGCTTTAACCACTGTTCTGAAGAGAGTTTGTGCCCCTTAGAGCGCCCGCACCTTGAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R R G D A F Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  480 CTCCTCAGCTTGCGGGGGGATTGCGATTAGGCACTTAAGGGTTGTCTGCAGGAGGATGTGTGGGGGATGCGGGGCGCTGCGGGGGGGG   | PAGAMAGN TRAGGGAAAGGGCCTCGSAGGGAAGGTCATTCATCGTANTGGACGGATCGATTCTCAGGGACGGGATAGCTCCTCTTCCAGGGAGCCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D B D K L L Y H L S R E P M V  A H Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACAAGCTTACGGCTCTGGGAGTTGTATATCCTCTTTAGCCAGAGGAGCCCTTTAGAGCCCCGCACCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGGATTGCGCTTTAACCACTGTTCTGAAGAGAGTTTGTGCCCCTTAGAGCGCCCGCACCTTGAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R R G D A F Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  480 CTCCTCAGCTTGCGGGGGGATTGCGATTAGGCACTTAAGGGTTGTCTGCAGGAGGATGTGTGGGGGATGCGGGGCGCTGCGGGGGGGG   | PAGAMAGN TRAGGGAAAGGGCCTCGSAGGGAAGGTCATTCATCGTANTGGACGGATCGATTCTCAGGGACGGGATAGCTCCTCTTCCAGGGAGCCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D B D K L L Y H L S R E P M V  A H Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACAAGCTTACGGCTCTGGGAGTTGTATATCCTCTTTAGCCAGAGGAGCCCTTTAGAGCCCCGCACCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGGATTGCGCTTTAACCACTGTTCTGAAGAGAGTTTGTGCCCCTTAGAGCGCCCGCACCTTGAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R R G D A F Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  480 CTCCTCAGCTTGCGGGGGGATTGCGATTAGGCACTTAAGGGTTGTCTGCAGGAGGATGTGTGGGGGATGCGGGGCGCTGCGGGGGGGG   | PAGAMAGN TRAGGGAAAGGGCCTCGSAGGGAAGGTCATTCATCGTANTGGACGGATCGATTCTCAGGGACGGGATAGCTCCTCTTCCAGGGAGCCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D B D K L L Y H L S R E P M V  A H Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACAAGCTTACGGCTCTGGGAGTTGTATATCCTCTTTAGCCAGAGGAGCCCTTTAGAGCCCCGCACCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGGATTGCGCTTTAACCACTGTTCTGAAGAGAGTTTGTGCCCCTTAGAGCGCCCGCACCTTGAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R R G D A F Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  480 CTCCTCAGCTTGCGGGGGGATTGCGATTAGGCACTTAAGGGTTGTCTGCAGGAGGATGTGTGGGGGATGCGGGGCGCTGCGGGGGGGG   | PAGAMANT TRAGEGRAMAGE CCTC GEAGGRAMAGE TATE TO THE TERM AND THE RESIDENCE TO THE CASE OF A MILLY HIDE REPORT OF THE RESIDENCE OF A MILLY HIDE REPORT OF THE RESIDENCE OF A MILLY HIDE REPORT OF THE RESIDENCE OF T | PAGE AGAINSTITAGEGAAAGSCCTCESSAGGGAATGATCATCTETATGGACGGGATCGATAAGACCCTTTCCAGGGAAGSCGCAAAGCCCCTTTCCAGGGAGCCCAATGTGGATCAGGAGCCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGAGAACCAATGAGGATCAGGAACCCAAAGGAACCAATGAGGAACCCAATGAGGAACCCAAAGAGAACCAATGAGGAACCCAAAGAGAACCAATGAGACCCAATGAGGAACCAAGAACCAATGAGGAACCAAAACAAC                
   | PAGAMAGN TRAGGGAAAGGGCCTCGSAGGGAAGGTCATTCATCGTANTGGACGGATCGATTCTCAGGGACGGGATAGCTCCTCTTCCAGGGAGCCCAATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D B D K L L Y H L S R E P M V  A H Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCACAAGCTTACGGCTCTGGGAGTTGTATATCCTCTTTAGCCAGAGGAGCCCTTTAGAGCCCCGCACCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGTTGGATTGCGCTTTAACCACTGTTCTGAAGAGAGTTTGTGCCCCTTAGAGCGCCCGCACCTTGAC E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R R G D A F Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  480 CTCCTCAGCTTGCGGGGGGATTGCGATTAGGCACTTAAGGGTTGTCTGCAGGAGGATGTGTGGGGGATGCGGGGCGCTGCGGGGGGGG  | PAGE AGAINSTITAGGGAAAGGGCCTCGGAGGGAATGATCATCTGTAATGGAGTAGAAACCCTTTCCAGGGAGGG   | PAGE AGAINSTITAGEGAAAGSCCTCESSAGGGAATGATCATCTETATGGACGGGATCGATAAGACCCTTTCCAGGGAAGSCGCAAAGCCCCTTTCCAGGGAGCCCAATGTGGATCAGGAGCCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGGATCAGGAGACCCAATGTGAGAACCAATGAGGATCAGGAACCCAAAGGAACCAATGAGGAACCCAATGAGGAACCCAAAGAGAACCAATGAGGAACCCAAAGAGAACCAATGAGACCCAATGAGGAACCAAGAACCAATGAGGAACCAAAACAAC  | PAGAMANT TRAGEGRAMAGE CCTC GEAGGRAMAGE TATE TO THE TERM AND THE RESIDENCE TO THE CASE OF A MILLY HIDE REPORT OF THE RESIDENCE OF A MILLY HIDE REPORT OF THE RESIDENCE OF A MILLY HIDE REPORT OF THE RESIDENCE OF T | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TEGRATIGNOGECTICCAGGAGGGGAATGGATCAGTAGGACCTTTCCAGGGAGGG  | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   
  | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A M Y A K G V L K R D H V H D A V R T N Y G R K L M P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTCCAACACCTTAGGCTCGCTGCAACACCTGGGGGTTATATCCTTTTAGGCCAAGCCCCAACTGTGGG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACACTTAGGGTTTAACGCCGTTCTGCGAACACGATGTTGTTGCCCGGGGCCTGGGGGCCCAAGCGTTATAGGCCCCGGGGCCTAACGGGGACCCCAAGCTTAAGGGTTCCTCTGCAACACCATTTTAAGCACCGTTCCTGCAACACCATTTTAAGCACCATTTTAAGCACCCTTTAAGGCAATTTTAAGCACCTTCGGAATTTAAGGATGTTTGTCCCGGGGCCTGAGGGTTAAGGGGACCCTAATGGGGACCCCAAGCTTTAAGGCAAGTTTTAAGCACCACTTTAAGGCAAGTTTTAAGGCAGTTTAAGGCAGTTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCTTTAAGGCAGTTTGCAAGAGTCCTTCCAGGGGGGTTAACGCAGGGGTTTAAGGCTTGAGGGTTTAAGGCAGTTTGAGGAATTTGAGACAGTTTGAGGAATTTGAGGAGTTTAAGGAGTTTGAGGAGTTTAAGGAGTTTGAGGAG | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A M Y A K G V L K R D H V H D A V R T N Y G R K L M P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTCCAACACCTTAGGCTCGCTGCAACACCTGGGGGTTATATCCTTTTAGGCCAAGCCCCAACTGTGGG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACACTTAGGGTTTAACGCCGTTCTGCGAACACGATGTTGTTGCCCGGGGCCTGGGGGCCCAAGCGTTATAGGCCCCGGGGCCTAACGGGGACCCCAAGCTTAAGGGTTCCTCTGCAACACCATTTTAAGCACCGTTCCTGCAACACCATTTTAAGCACCATTTTAAGCACCCTTTAAGGCAATTTTAAGCACCTTCGGAATTTAAGGATGTTTGTCCCGGGGCCTGAGGGTTAAGGGGACCCTAATGGGGACCCCAAGCTTTAAGGCAAGTTTTAAGCACCACTTTAAGGCAAGTTTTAAGGCAGTTTAAGGCAGTTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCTTTAAGGCAGTTTGCAAGAGTCCTTCCAGGGGGGTTAACGCAGGGGTTTAAGGCTTGAGGGTTTAAGGCAGTTTGAGGAATTTGAGACAGTTTGAGGAATTTGAGGAGTTTAAGGAGTTTGAGGAGTTTAAGGAGTTTGAGGAG | 240 EK I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  241 TECATTGTAGGCCTTCCACCAGGTAGGCCGATGTG  242 TECATTGTAGGCCTTCCACAGGTAGGTAGACTCGGCGTGTCTTAGGTAGG   
  | 240 EK I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L M P P D T E G R V A G R L K L  241 TECATTGTAGGCCTTCCACAGCTCAGGCTGAGATGGGCGGGGGGGG   | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TECATTETAGECTITCCACAGCTACGETCAGGAACTGGGCCATGGGGGGGGGGG   | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TECATTETAGECTITCCACAGCTACGETCAGGAACTGGGCCATGGGGGGGGGGG   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A M Y A K G V L K R D H V H D A V R T N Y G R K L M P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTCCAACACCTTAGGCTCGCTGCAACACCTGGGGGTTATATCCTTTTAGGCCAAGCCCCAACTGTGGG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361
GAGATCCTGAACACTTAGGGTTTAACGCCGTTCTGCGAACACGATGTTGTTGCCCGGGGCCTGGGGGCCCAAGCGTTATAGGCCCCGGGGCCTAACGGGGACCCCAAGCTTAAGGGTTCCTCTGCAACACCATTTTAAGCACCGTTCCTGCAACACCATTTTAAGCACCATTTTAAGCACCCTTTAAGGCAATTTTAAGCACCTTCGGAATTTAAGGATGTTTGTCCCGGGGCCTGAGGGTTAAGGGGACCCTAATGGGGACCCCAAGCTTTAAGGCAAGTTTTAAGCACCACTTTAAGGCAAGTTTTAAGGCAGTTTAAGGCAGTTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCAGTTTAAGGCTTTAAGGCAGTTTGCAAGAGTCCTTCCAGGGGGGTTAACGCAGGGGTTTAAGGCTTGAGGGTTTAAGGCAGTTTGAGGAATTTGAGACAGTTTGAGGAATTTGAGGAGTTTAAGGAGTTTGAGGAGTTTAAGGAGTTTGAGGAG | 240  E K I R E R A S E 6 K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TORCATTICAGEAGACTICACCAGACTAGACCACTICAGACTAGACCACTICAGACTAGACCACTICAGACTAGACCACTICAGACTAGACCACTICAGACTAGACCACTICAGACTAGACT  | 240 EKIRERASE EKNIIVNO DAVRITUS ROBORKACCITICCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGGACCCATTETCAGGACCCACCTTICACCACCTTICCAGGGACCCACCTTICAGCACCTTICAGGACCACCTTICAGGACCACCTTICAGGGACCCCAGCCTTAGGGACCCCCAGCCTTAGGGCCCCCCCAGCCTTAGGGCCCCCCCAGCCTTAGGGCCCCCCCC   | 240  E K I R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A H Y A K G V L K R D H V H D A V R T H Y G R K L H P P D T E G R V A G R L K L  1241 TGCATTGTGGGCCTTTCCAACAGCTTACGGTCGTACGTCGTCTACGGCTGTTATACCTCTGTTTAGCCCAGGTGGGTTGTTTCCACCCTTTCCACCGAGCTTGAG  C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  480  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTTCCTGGAAGAGGATGTTGTGCCCCCTGGGGGCCCCAGCGTAATGGGGAACGCAGCTTTAGCCCTTGAC  E I L H Y R V E H A F N D G V L E D D V V P L C A A L A A Q R H G D A R Y A L D  481 CTCCTCCAGCTCGCGGCGCATATGCGATAAGGCACCTTAAGGGTGTTCTCAGTGGTTCTAGTGTTAAGCACGACTTGAGGTGACTGAGGGGAACGAGATGTTGACCTTCAGTGGTTCAGTGGTCTCAGTGGTCTCAGTGGTCTCAGTGGTCTCAGTGGTCTCAGTGGTCTCAGTGGTCCACCTGAGGTGACTGAC   | 240  241 GAGAAGATTAGGGAAAGGGCCTGGAAGGAAAAAAAGATGATCATGTAATGGACGAGATCGATAAGACCCTTTCCAGGGACGGGATAAGCCCCTTTCCAGGGACCGATTGTG  241 R E R A S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTCCGCTCATGGGCATGGCGCATGTGGGGATTTATACCTTAAGCCCAAGAAGATTCCCCCCTTACAACGCCCCCCCACGCTTGAG  C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACCACGGTTCTCTGGAACAGGAGTGTTGTGCCCTTGACCACGCCCCCACGCGTTTAAGCCACGGTATGGGGACAATGGCCCTTGACCACGGTTTCACGACGTTCACGTTCACGGTAGGGCACTCAGGGTTAGGTTCAGGTTAGGTTCAGGTTGAGGTTCAGGTTTGAGCAGTTAGGTTCAGGTTTCAGGTTCAGGTTTCAGGTTCAGGTTCAGGTTTCAGGTTCAGGTTGAGGTTCAGGTTGAGGTTGAGGTTGAGGTTCAGGTTGAGGTTGAGGTTGAGGTTCAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTAGGTTTCAGGTTTCAGGTTTCAGGGGAACCCAGAAACCAGAAACCAGAAACCAGAAACCACC  | 240  R R R R R S E G K M I I V N D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCATCCCTTTCCAGGCAGCCTTAGGCCCCCCAGCCTTAGGCCCCCCCAGCCTTAGGCCCCCCCAGCCTTAGGCCCCCCAGCCTTAGGCCCCCCCC  | 121 GAGAAGATTAGGGAAAGGCCTTGGAGGGAAAGATGATTAGTGATAGGCAGATGATAGACCTTTCCAGGGACGGGATAAGCCCCCTTCACCACCTTTCCAGGGACCGATGTG E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 GGATTGTAGGCCTTTCCAACAGCTTACGGTCATGGAGTCGGACTGGAGTCGATTAGTCTCTGTTTAAGCCACGTTCGCCCCTTACAGCGCCCCCCCAGCTTGAG C C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  480 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTACCACGGTGTCCTGGAAGACGATGTTGCCCCTTGAGCGCCCCCAGCGTAATGGGGACCCCCACGTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCCCAGCTTGCGGCGGGATATGGCAGTTAGGGGTTTTGCAGTGTTGTCAGTGAGTCTGAGTCTGAGTGCAGTGTGAGGTCTGAGGTTGTAGAGCAGG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E C L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  721 AGGGGACACCAGAGAGTCCTCCTGTGAGGCATTGAAGCCCGCCTTGAGGTTAGCCCTTGAGATTATAGGAGTATATTGGGAACTCTCCTGTGAGGGACTTGAGGCCTTGAGGCTTGAGGTTGGGTTAGAGCAG  840 A T I A R R L S Q L L R E L L Y G L V E I E V V G R G R G R G V N M N V V P S S S  841 ATTGACCCTGACCCCATGCTTGAGGCCATTTGAGCCATTTTTTCCCTCTTGAGGGCATTTTTTGGAGGTTAGAGCAGTTTTTTTT   
   | 121 GAGAMATTAGGGAAAGGCCTCGGAGGGAAAGATTATCCTGTATGGACGAGATCGATAMGACCCTTTCCAGGGAGGATAAGCCCCTTCCAGGGAGCCGATGTG EKIRERASEGKMIIVNDEIDKTLSRDGDLYBAAGATGATGATGAGATAGACCCTTTCCAGGGAGACCGATTCCACACCTTTCCAGGGAGCCGATGTG EKIRERASEGKMIIVNDEIDKTLSRDGCATAGGCCGACTGAGGATAAGACCTTCTCCAGGGAGACCAGGAGGAGAAGAGTTTCCCCCCTTACCACCCTTCCAGGGATAGAGCCCCCCCC   | 240  241 TGCATGTGAGGGAAGGGCCTTGGAGGGAAGGATGATGATCGTAATGGACGAGATCGATAGGACGGGGATGAGGCCCCTTCTCACCACCTTTCCAGGGGAGCGGAAGGCCGAATGTG  241 TGCATGTGAGGCCTTTCCAACAAGCTTACGGTCATGGGGAACTGGAGGGTTATATCTTCGTTTAAGCCAGGAGGGATCAGTTTCGCCCTTACAACCCCCTTGAGCCCCCCGCAGCTTGAG  242 TGCATGTGAGGCCTTCCAACAACCTTACGACGACTGAGGAACTGAGTTGATGCTTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAACCCCCCCC  | 240  240  241  241  241  241  241  242  241  242  241  243  242  243  244  244  | 240 241 GAGAAGATTAGGGAAAGGGCCTGGGAGGGAAAGTGATCATGGTAATGGACGAGATGGATAAGACCCTTTCCAGGGAGGG   | 240 241 GAGAAGATTAGGGAAAGGGCCTGGGAGGGAAAGTGATCATGGTAATGGACGAGATGGATAAGACCCTTTCCAGGGAGGG   | 240  240  241  242  243  244  245  246  247  248  248  249  249  249  249  249  240  240  240  | 240  240  241  242  243  244  245  246  247  248  248  249  249  249  249  249  240  240  240  | 240  241 TECRITICAGEGRAAGEGECCTCEGAGEGRAAGATGATCATCETAATGGACGAGATCGATAAGACCCTTTCCAGGGAGGGGATAAGCTCCTCTACCACCTTTCCAGGGAGGCGAATGGTEER  241 TECRITICAGCCCTTTCCAACAAGCTTACGGCTCTGGCACTCGGGATCGGGTTAATCCTCTTTAACCCAAGGAAGAAGATCTTCCCCCCTTAACGCCCCCCCAACCTTCAGGCCCCTTCAACACCCCCCCC  
   | 240  241 TISCATTAGGGGAAAGGGCCTCGGAGGGAAAGATGATCATCGTAATGGACGAGATCGATAAGACCCTTTCCAGGGGAGGGGATAAGCTCCTCTACCACCTTTCCAGGGGAGCCGAATGTG  242 EKIRERASEGKHIIVNDEIDKTLSRDGBCAACGAGTCGATAAGGACCGATCAGGGATCAGGGGGATAAGCTCCTCTACCACCCTTTCCAGGGGAGCCGAGCTCAGGGATCAGGATCAGGATCAGGGATCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTAGCCCCCTAACAGGACCAGTTCAGCCCCCTAACAGCACCACTTGAG  241 TIGCATTCAGGCCTTCCAACAAGCTAGCGCTATCAGGCCACTCAGGCACTCAGGACTCAGGACTAAGCACACAGACCAGTATCCCCCTGACCACCCCCAACCTTCAACCACCCCCCCAACCTTCAACCACC  | 240  241 TISCATTAGGGGAAAGGGCCTCGGAGGGAAAGATGATCATCGTAATGGACGAGATCGATAAGACCCTTTCCAGGGGAGGGGATAAGCTCCTCTACCACCTTTCCAGGGGAGCCGAATGTG  242 EKIRERASEGKHIIVNDEIDKTLSRDGBCAACGAGTCGATAAGGACCGATCAGGGATCAGGGGGATAAGCTCCTCTACCACCCTTTCCAGGGGAGCCGAGCTCAGGGATCAGGATCAGGATCAGGGATCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTAGCCCCCTAACAGGACCAGTTCAGCCCCCTAACAGCACCACTTGAG  241 TIGCATTCAGGCCTTCCAACAAGCTAGCGCTATCAGGCCACTCAGGCACTCAGGACTCAGGACTAAGCACACAGACCAGTATCCCCCTGACCACCCCCAACCTTCAACCACCCCCCCAACCTTCAACCACC  | 240  240  241  242  243  244  245  246  247  248  248  248  249  249  249  249  249  | 240  241 TISCATTAGGGGAAAGGGCCTCGGAGGGAAAGATGATCATCGTAATGGACGAGATCGATAAGACCCTTTCCAGGGGAGGGGATAAGCTCCTCTACCACCTTTCCAGGGGAGCCGAATGTG  242 EKIRERASEGKHIIVNDEIDKTLSRDGBCAACGAGTCGATAAGGACCGATCAGGGATCAGGGGGATAAGCTCCTCTACCACCCTTTCCAGGGGAGCCGAGCTCAGGGATCAGGATCAGGATCAGGGATCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTCAGGACTAGCCCCCTAACAGGACCAGTTCAGCCCCCTAACAGCACCACTTGAG  241 TIGCATTCAGGCCTTCCAACAAGCTAGCGCTATCAGGCCACTCAGGCACTCAGGACTCAGGACTAAGCACACAGACCAGTATCCCCCTGACCACCCCCAACCTTCAACCACCCCCCCAACCTTCAACCACC  | 240  241 TECRITICAGEGRAAGEGECCTCEGAGEGRAAGATGATCATCETAATGGACGAGATCGATAAGACCCTTTCCAGGGAGGGGATAAGCTCCTCTACCACCTTTCCAGGGAGGCGAATGGTEER  241 TECRITICAGCCCTTTCCAACAAGCTTACGGCTCTGGCACTCGGGATCGGGTTAATCCTCTTTAACCCAAGGAAGAAGATCTTCCCCCCTTAACGCCCCCCCAACCTTCAGGCCCCTTCAACACCCCCCCC  | 240 241 TREAT A SEG K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  241 TREAT A SEG K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  242 TREAT A SEG K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  243 TREAT A SEG K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  244 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  245 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  246 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  247 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  248 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  249 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  240 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TREAT A SEG K M I I V M D A V R T N Y G R K L N P P D T E G R V A G R L K L  242 TREAT A SEG K M I I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  243 TREAT A SEG K M I I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  244 TREAT A SEG K M I I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  245 TREAT A SEG K M I I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L
E  246 TREAT A SEG K M I I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  247 TREAT A SEG K M I I V M D N I G S L V I N M N Q A R R E R G L T I P V G P I G K V  248 TREAT A SEG K M I I V M D N I G S L V I N M N A T D E V E V E F I R R S I E Q  249 TREAT A SEG K M I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  240 TREAT A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  240 TREAT A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R S I E Q  240 TREAT A SEG CALACACACACACACACACACACACACACACACACACAC  | 240 E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCATTCCAACAGCTTACGCTCTGAACAGCCATTGTGCCGCCTTGTCAAGCCACCTTGAGGCCCGCACCTTGAGGCCCGCACCTTGAGGCCCGCACCTTGAGGCCCTTAAGCCAACGCCCCCAACCTTGAGGCCCGCAACCTTGAGGCCCTTAAGCCAAGGCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCAACCTTGAGGCCCTTAAGCCAACGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCCCCCAACCTTGAGGCCTTGACCAACCA  | 240  E K I R E R A S E G K M I I V M D E I D K T L S R D G D K L L Y H L S R E P N V  A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TEGATTGTAGECCTTTCCAACAGCTTCGETGACTGEACATCGEGGTGTTATATCCTTTTAGCCAAGGTGTGTGTGTGTGCCCCTTACAGCCCCCCCC   | PAGE AGAINSTITAGGGAAAGGGCCTCGGAGGGAATGATCATCTGTAATGGAGTAGAAACCCTTTCCAGGGAGGG   | PAGE AGAINSTITAGGGAAAGGGCCTCGGAGGGAATGATCATCTGTAATGGAGTAGAAACCCTTTCCAGGGAGGG   | PAGE AGAINSTITAGGGAAAGGGCCTCGGAGGGAATGATCATCTGTAATGGAGTAGAAACCCTTTCCAGGGAGGG   | 121   GRAMAGN TIANGGRAMAGEGGCTTGAGGGAMAGATATTATICTICTATGSCAGATAGACCTTTCAGGGCAGGGATACCTTCTCAGGACCCTATCCAGCATATGT   240   241   141   241    |
| A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K  241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGCTCATGACCGCCCCCCCC   | H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  CATEGACATGATCGGCGACTCGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAAGCGCCCCCGCAGCTTGAG  M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  TAACGACGGTGTCCTGGAAGACGATGTTGGCCACTGTGGCGGCCCGCAGCGTTATGGGGGAAGCCAGTATGGGGAAGACCATTGACC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GCAGCTTAAGGGTTGTCAGTGAGTCTGATGTGAGGTGGCGACTGAGGGTGAGGTTGAGGTTGAGGTTGAGCTTATCAGCCAGGAGAAG  D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  CSTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATGAGGAGTACAACAAGATGGCCGAGGGGGGACCAGTGAGGAGTTGAGCTTTGCCCTCT  V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M ORFR:  ACTTGAACTCTATGGCCTTGTGCAGATTGAGGTTGCGGGGGGCGACGGGGGGGG  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  1 TGCATTGTAGGCCTTTCCAACAGCTTAGGCCTATGGAGTGGGGGGGTGGGGTGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTGGCCCCTTACAGGGCCCCGCAACCTTGAG  241 TGCATTGTAGGCCTTTCCAACAGCTTCAGGTCAGGCGACTGGGGGTGTTATATCCTTCGTTTAAGCCAAGGAGGATCAGTTTGGCCCCTTACAGGGGCCCGCAACCTTGAG  260 C I V G L S N K L T V M O N I G O S G V I S S F K P R R I S F A P Y S A P Q L E  261 L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  262 GAGATCCTGAACTACAGGGTTGAAGATGCGCTTTAACCACGGTTCTGGAAGAGCATGTTGTGCCTGGGGGCCCTGGGGCCCAGGCTAATGGGGGACCAGTTATCGCTTGACCAGGGCTAATGGGGGGCCCAGGCTAATGGGGGACCAGTTTATCACCTAGGGGGCCCAGCGCTAATGGGGGGCCCAGCGCTAATGGGGGGCCACGCGCTAATGGGGGGCCAACCAGTTTTTCAGCCAGGGCCACCTCGAAGAGTACGGGCGCTCAGGGCCCAACCAGAGATCTTTTAACGACCAGTATGGGGGCAACCAGAAGATCCTCCTGGAAGAGAGTCTCTGGAGGATGAGGGGGGGCACCTGGAAGTAACAAGAGTGCCCCACTGGAGGATATATAGGAAGATCACAGAGAGTCTTTCCAGCCCTCCAGGGGGGGTAACCAGGGGCCACCTGAAGATACAACAAGATGCCCCCACTGGAGATATATAGGAAGTACACAAGATGCCCCACTGGGGCCACCCCCACCAGGGGCGTGCACCCCACTGGAGATATATAAGGAAGTACAACAAGATGCCCCCACTGGGGCCACCCCCACCAGGGGCCTGGGAACTTCCACCTCCAGGGGGGTAACCAGGGGCCTGGGAACTACAAAGATGCCCCACTGAAGATCCTCCAGGGGCAACCTCCAACCTCATAGGGGTCACCCCACTCGAAGTACCAGGGGCCCTGGGAACTTCCAACCTCATAGGGGTCACCCCACTCGAACTTCCACCTCCAGGGGCCACCCTCCATGGGGGCTAAGGGGAACCTTTCACCTCCAGGGGCCACCCCCATTTTTCCACGGGGCTAACCAGGGGCCTGGGAACTTCTAACCTCAGGGGCTAACCACACCCCATTTTTTCCACGGGCCAACCTCCAACCCCCATTTTTCCACGGGGCAACTTTTTCCCTTGAGGGCTAACCACGGGGCCTGGGAACTTTTAACCTTAAGGGGTGTTGTT GCGGGCAACCTTTTTTCCACGGGGCAACTTTTTCCCTTCTGAGGGCCACCCCCATTTTTTCCACGGGGCAACTTTTTCCAGGGGGAACTTTTTTCCAGGGGCTAACCACCCCCATTTTTTCCACGGGGCAACTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCCAGGGGGAACTTTTTTCACAAAACACTTGCACCCTGAACTGCACCCCCATTTTAAGGGGCTAACCACCACCACTTTTTCCACGGGGAACTTTTTCCAGGGGGAACTTTT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTTCCAACAGCTCAGGCCACTGAGGCCACTGAGGCCACTGAGGCCCCCCACCTTCAGGCCCCCCCACCTTCAGGCCCCCCACCTTCAGGCCCCCCACCTTCAGGCCCCCCCACCTTCAGGCCCCCCCACCTTCAGGCCCCCCCACCTTCAGGCCCCCCACCTTCAGGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGACGACTGGGGTGTTATATCCTTCTTTAGGCAAGGACGACTCAGTTTGGCCCCCCCAAGCTTGAG C I V G L S N K L T V H D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACGACGGTGTCCTGGAAGAGGATGTTGTGCCCCTGGGGGCCCCGGGGCCCAGGGTTGAGGGGGGGG   | A N Y A K G
V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGEACCACTGGGGTGTTATATCCTTCATTTAGCCAAGCAGGATCAGTTTGGCCCCCTTACAGCGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGEACCACTGGGGTGTTATATCCTTCATTTAGCCAAGCAGGATCAGTTTGGCCCCCTTACAGCGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGEACCACTGGGGTGTTATATCCTTCATTTAGCCAAGCAGGATCAGTTTGGCCCCCTTACAGCGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGEACCACTGGGGTGTTATATCCTTCATTTAGCCAAGCAGGATCAGTTTGGCCCCCTTACAGCGCCCCCCCC  
   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG   | A N Y A K G V L K R D N V N D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTASGCCTTTCCAACAAGCTTACGGTCATEGEACATGATCGGCCAACTCTGGGTCTTATATCCTCTTTTAGCCAAGSAGGATCAGTTTCGCCCCCTTACAAGCCCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACACGGTCTCCTGGAAAGAGTGTTGTCCCACTSTCGCCGGCCCCAGCGTAATGGGGAACCCCTGAATGGGGAACCCTTAACAGGTTGAACCACGTTGTCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAAGGTTGAGGTTGAGGTTGAGTTTAAGACCAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  601 TTGAGGGACAACCAGAAGATCCTCCTGTAGCGCCTCCAGGGGGGGTACCCCCCACTGAGATTATACAGGAACTGACACAAGAAGAACCGTTTGGGGGGACCCCCCCATGGAGGTATATATA  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG  
  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGGGTTAGAGCAGGTTGCTCTGCAAGAGGATGTTGTCCCCTGCGGGGCCCAGGGTCAAGGGGGAAGCCCTGAGGGGAACCCTTAGAGGTTGAGCAGGGTTGAGACGGTTGAGCACGGTTTAGAGCAGGTTGTCCCTTGCAAGAGGTTGTCCCTTGCAAGAGGATGACGAGTTGAGAGATGACGAGGTTGAGAGATGAGGAGGATCACAGAGAGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D N V N D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTASGCCTTTCCAACAAGCTTACGGTCATEGEACATGATCGGCCAACTCTGGGTCTTATATCCTCTTTTAGCCAAGSAGGATCAGTTTCGCCCCCTTACAAGCCCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACACGGTCTCCTGGAAAGAGTGTTGTCCCACTSTCGCCGGCCCCAGCGTAATGGGGAACCCCTGAATGGGGAACCCTTAACAGGTTGAACCACGTTGTCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAAGGTTGAGGTTGAGGTTGAGTTTAAGACCAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  601 TTGAGGGACAACCAGAAGATCCTCCTGTAGCGCCTCCAGGGGGGGTACCCCCCACTGAGATTATACAGGAACTGACACAAGAAGAACCGTTTGGGGGGACCCCCCCATGGAGGTATATATA  
   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACTGCGCCTGCTTATATCCTCGTTTATAGCCAAGCAGGATCCASTTTCGCCCCCTTACAGCGCCCCCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGACTCTGAATCAAGGGTTGGAATGCGTTTAAGCACGGTGTCTCTGCAAGAGGATGTTGTCCCCTGCGCGCCCCTGAGGGTCAAGGGGGAACCCTTGACG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGGTTGAGGGTTGAGGTTGAGGTTGAGGGTTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGCCAGGGCCAGGTTGAGGGGCAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGGCAGGCCCATTGTAGGGGCTAGGGCCATTTTAGGGGGTTGAGGGTTGAGGGTTGAGGGGCAGGGCCATTTTGAGGGGCTAGGGCCATTTGAGGGGCAGGCCCATTTTAGGGGGGGAGAGGCCCATT | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT  
  | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   
   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAGCACGGTTCAAGCAAGGAGGAGTGTGTGT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTGACTGGCGACTTGGGCGACTGGGGGTGTTATATCCTTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCCTAACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N 0 N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  450 GAGATCCTGAACTACAGGGTTAACGACGGTTCAAGCAAGGAGGATGTTGTGCCCGGCGCCCGGGCCCGGGCCCAGGGTAGGGGACCCCGGTAGGCGTTGAGCCCTGACGGGTTCAGGGGTTCAGGGATGGGGGAAGACGGTTGTGGGCGCCGGCCCGGGCCCAGGGTAGGGGACGCCAGTATGGGGATGGGGTAGCCCTGACGCGCGCCAGAGAGGATGTGGGGCGCCGGCCCGGGCCCAGGGTAGGGGATGGGGGAGCCCCTGTACGCGCGCCCATGAGATGAGGGTAGGGATGGGGATGCCCCATGAGATGAGGTGGGGCCCAGCGCAGTATTGCAGCATTACAGCAGGTTGAGTTTGAGCTGAGTTCTCAGGTGGGGCCCAGCTGAGGGCCCAGCTGAGGGTAGGGGATGCCCCCATGAGATGAGCTGAGTTGAGGTTGAGGTTTGCAGGTTGAGTTTTACAGGATGGGGAACCAGAAACACAAGATCCCCCAGTAAGGCGCCATGAGGAGGATGAGCCCCCCTCTGAGATATATAGGAAGTACAACAAGATCCCCCGCGCGATATTGCAGTAGAGCACCAAGAAGTCCCCCCATGAGATGAGCACCAAACAAGAAGTCCTCCTGTACGCCGCTGCAGAATTAGGAATTAACGAAGTACAAGAAGTCCTCCTGTACGCCGCTGTAGGAATTAAGGATGGGGCCCGCCGCGCGCG  | A N Y A K & V L K R D N V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTGACATCATGGCGACTGGGGGACTGGGGTGTTATATCCTTCAGGCAAGAGGACTCAGTTTCGCCCCCTAACAGGCCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGATCCTGAACTACAGGGTTCAACGACGTTCAGGCAAGAGCAGTGTTGTGCCCGCGGCCCGGGCCCGGGCCCGGGAGCCGGATGGGGGATGCGCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCACCTTCCCGCGCGATATTCCCATAAGCCACTTCAGGGCTTCTGGAGTCTGTGAGTTCTATGTGAGCTGAGCTGAGCTGAGCTGAGCTTAAGTTTACCAGAG C T N A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N E L L L K P A V G E  601 TTGAGGGGAACCCAGAAGTCCTCCTGTAGGCCCTCCAGGGGGGTTACCCCCCACTGAGATTATATGGAGTTACACAAGATTCGGGGCCTTCTCTCTTCTCCTCT T Q R R L S Q L L Y A V M T S Q G G Y P T E I Y R K Y N K M A E E Q F G 8 N A L  721 ACGCAGAGGAGGCTTCCCAGGCACCTTGAAGGGCACTCTGAGGGCCTTGTCTGAGTTGTGAGTTCTGCGGGCCCGCTGGCCGCTGAGTATTCCCTCTTCTCCTCTCTCT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTATGTGGCCGATTGGGCGATTGTATACCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I Y G L S N K L T Y N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAAACGACGGTTCAAGCAAG  | A N Y A K & V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGCCACTCGGGTGTTATATCCTTCAGGCCAAGAGAGCAGTTTCGCCCCCTAACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGACTCTGAACTACAGGGTTCAAGAGCGTTCAGGCAAGAGCAGTTCTGGCCGGCC   
   | A N Y A K & V L K R D N V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTGACATCATGGCGACTGGGGGACTGGGGTGTTATATCCTTCAGGCAAGAGGACTCAGTTTCGCCCCCTAACAGGCCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGATCCTGAACTACAGGGTTCAACGACGTTCAGGCAAGAGCAGTGTTGTGCCCGCGGCCCGGGCCCGGGCCCGGGAGCCGGATGGGGGATGCGCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCACCTTCCCGCGCGATATTCCCATAAGCCACTTCAGGGCTTCTGGAGTCTGTGAGTTCTATGTGAGCTGAGCTGAGCTGAGCTGAGCTTAAGTTTACCAGAG C T N A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N E L L L K P A V G E  601 TTGAGGGGAACCCAGAAGTCCTCCTGTAGGCCCTCCAGGGGGGTTACCCCCCACTGAGATTATATGGAGTTACACAAGATTCGGGGCCTTCTCTCTTCTCCTCT T Q R R L S Q L L Y A V M T S Q G G Y P T E I Y R K Y N K M A E E Q F G 8 N A L  721 ACGCAGAGGAGGCTTCCCAGGCACCTTGAAGGGCACTCTGAGGGCCTTGTCTGAGTTGTGAGTTCTGCGGGCCCGCTGGCCGCTGAGTATTCCCTCTTCTCCTCTCTCT   | A N Y A K & V L K R D N V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGCTGACTGGCGACTTGGGCGACTGGGGGTGTTATATCCTTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N 0 N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  450 GAGATCCTGAACTACAGGGTTAAGCACGTGTAAGCGAAGGAAG   | A N Y A K G V L K R D N V N D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTASGCCTTTCCAACAAGCTTACGGTCATEGEACATGATCGGCCAACTCTGGGTCTTATATCCTCTTTTAGCCAAGSAGGATCAGTTTCGCCCCCTTACAAGCCCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACACGGTCTCCTGGAAAGAGTGTTGTCCCACTSTCGCCGGCCCCAGCGTAATGGGGAACCCCTGAATGGGGAACCCTTAACAGGTTGAACCACGTTGTCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAACCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAAGGTTGAGGTTGAGGTTGAGTTTAAGACCAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  601 TTGAGGGACAACCAGAAGATCCTCCTGTAGCGCCTCCAGGGGGGGTACCCCCCACTGAGATTATACAGGAACTGACACAAGAAGAACCGTTTGGGGGGACCCCCCCATGGAGGTATATATA   | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC   | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC   
  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TSCATTGTAGECCTTTCCAACAAGCTTACGGTCATEGACATGACCGCCCTCCCGCTGCTTATATCCTTCTTTAAGCCAAGCAGCTCGCCCCCCCAACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGCTTTAACACGGTCTCTGGAAGACGATGTTGTGCCCACTGCGGGGCCCAGCGTTAATGAGGATGACCCTTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTTGGAGGATGGCGACTGAGGGTTGAGGTTGAGGTTGAGGTTTAAGGAGGACACCAGAAGAAGATCCCTCCTGGGGGGGACCCCCCACGTGAGAGTTGAGGACTGAAGGATGAGGAGGACACCAGAAGATTCCCCCTCTGAGGGGTGTCCCCCCACGTGAGATATTAAGGAACACACAGAGAGAG  | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TSCATTGTAGECCTTTCCAACAAGCTTACGGTCATEGACATGACCGCCCTCCCGCTGCTTATATCCTTCTTTAAGCCAAGCAGCTCGCCCCCCCAACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGCTTTAACACGGTCTCTGGAAGACGATGTTGTGCCCACTGCGGGGCCCAGCGTTAATGAGGATGACCCTTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTTGGAGGATGGCGACTGAGGGTTGAGGTTGAGGTTGAGGTTTAAGGAGGACACCAGAAGAAGATCCCTCCTGGGGGGGACCCCCCACGTGAGAGTTGAGGACTGAAGGATGAGGAGGACACCAGAAGATTCCCCCTCTGAGGGGTGTCCCCCCACGTGAGATATTAAGGAACACACAGAGAGAG  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTASGCCTTTCCAACAAGCTTACGGTCATGACTGCGCCCACTGGGGTTATATCCTTGTATACCTTGAGCACTGCCCCCCTTACAGCGCCCCCCCAAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTAGAGTAGCGCTTTAACGCGTGTCCTGGAAGAGGATGTGGGCGCCCCGCGGCCCCGCGGCCCCGGGGCCCAGGGTTAGGGGGAACTAGGGGTTAGCCTTGAC E I L N Y R V E M A F M D G V L E D D V V P P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGTTTAGGGTTGCAGTGAGGTGGGGAACTGAGGGTTGAGGTTGAGTTTAGGCAGG C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  601 TTGAGGGAACAACAGAGAGATCTCCTGTAGGCCTCAGGGGGGTGCCCCACTGGAGAGTGGCGAAGTGAGAGTTGAGGATGGGGGAAGATGCTCCTGGGGGGCTCCCCAGGGGGGGTTACCCCCAGGGGGGGCCCCACTGAGAGATGGTCGAAGAGTGCTCGAAGAGTGGCGAAGATGGCGCAACCAGAGAGAG   | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGACTGGGCCCCATGGGGTTATATACTTCTTTAAGCCAAGCAGCAGCTCGCCCCCCCAAGCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAATACAGGGTTGAAGGCGTTAACAGGGTGTCCTGGAAGAGGATCTGGTGGGGCCCCCGCGGCCCCGCGGCCCCGGGGCCCAGGGTTAGGGGGAGCAGGTTGACCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCTTTAGGGTGTGCCTGCAGGGACTGAGGGTGGGGAACTGAGGGTTGAGTTTAGGGTAGGGGTAGGGGAACTGAGGGTTGAGTTTAGGCAGG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  601
TTGAGGGAACACCAGAGAGATCTCCCTGTAGGCCTCCCAGGGGGGGCCCCACTGAGAGTTGAGAATGGCGCGAAGAGTGGCGAAGAGTGCCCCAAGGGGGGCCCACTGAGAGATGATCTGGGGGGCCCCCATGAGGGTTAACTAGGAAGTGGCCGAAGAGTGGCGAAGAGTGCCCCAAGGGGGGCCCCACTGAGAGAGTGCCCCAAGAGGAGGCTTACCTCCTATGGGGGGCCCCCACTGAGGATATATAGGAACTACAACAAGAGTGCCCCAAGGGGGCCCCCCACTGAGGATATTAGGAACTACACAAGAAGTGCCCCCACCCCCATGAGGATTGACCTCCTAGGGGGGCCCCCACTGAGGAATTATAGGAACTACACAAGAAGTGGCCGAGGGGGGTTTACTGGGGGGCCCCCCATGAGGATTATAGGAATTAAGGAAGTGCCCCAAGTGGGGGGGCCCCACTGAGGAGGCCTTCCCCAGCGCCCCACTGGGGGGGCCCCCACTGGGGGGCCCCCACTGGGGGGGCCCCCACTGGGGGGGCCCCCACTGGGGGGGCCCCCACTGGGGGGGCCCCCCCC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGCAGCCACTCGGGTGTTATATCCTCTTTAAGCCAAGCAGCAGCTCGGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGCAGCCACTCGGGTGTTATATCCTCTTTAAGCCAAGCAGCAGCTCGGCCCCCCCC  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC  | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TSCATTGTAGECCTTTCCAACAAGCTTACGGTCATEGACATGACCGCCCTCCCGCTGCTTATATCCTTCTTTAAGCCAAGCAGCTCGCCCCCCCAACCTTGAG C I V G L S N K L T V N D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTGCGCTTTAACACGGTCTCTGGAAGACGATGTTGTGCCCACTGCGGGGCCCAGCGTTAATGAGGATGACCCTTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGGTTGGAGGATGGCGACTGAGGGTTGAGGTTGAGGTTGAGGTTTAAGGAGGACACCAGAAGAAGATCCCTCCTGGGGGGGACCCCCCACGTGAGAGTTGAGGACTGAAGGATGAGGAGGACACCAGAAGATTCCCCCTCTGAGGGGTGTCCCCCCACGTGAGATATTAAGGAACACACAGAGAGAG  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TSCATTGTAGGCCTTCCAACAAGCTTACGGTCATGAACGGCCCTCGCGGCTCTATATGCTCTTTTAGGCCAAGGAGGATCAGTTCGCCCCTTACAGCGCCCCCCCC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241
T9CATTGTA9GCCTTTCCAACAAGCTTACGGTCATGEACATGATCGGCGACTCGGGTGTTATATCCTTCTTTAAGCCAAGCAGTCAGT   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTGGGCTCTTGGCGCACTCGGGGTGTTATATCCTCGTTTAAGCCAAGGAGCATCAGTTTCGCCCCTTACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAAGTACAGGGTTGAAGTGGCGTTTAACACGGTCTCTGGAAGAGCAGTGTTGTGCCGGGCCTCGGGGCCCGGGCCCAGGTATGGGGGACCAGGTTATGAGCAGGTTAACGGGTTAACAGGGTTGAACTGGCGTTTAACACGGTTCTGGAAGAGCAGTGTTGTCCAGTGGCCGCGCCCCGGGCCCCAGGGGACCAGGTATGGGCAGGTTAACGGGTTAACGGGTTAACGGGTTGAACTGAGGGTTGCCGTGAAGAGCAAGAGAGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTAGGCTCATGGCGACTTGGGCGACTTGGGGTGTTATATCCTCGTTTAAGCCAAGGAGCATCAGTTTGGCCCCTTACAGCGCCCGCC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCAACAGCTTAGGGTCATGEACATGATGGCGCACTCGGGGTTTATATCCTCGTTTAGCCCAAGGAGCATCAGTTTCGCCCCTTACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V H D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACACAGGTTGAAATGGCGTTTAACACGGTGTCTGGAACACGATGTTGTGCCTGGACCGCGCCCCCGCGCCCCGCGCCCAGCTATGGGGGCCCAGGTTATGGCATGACCAGGTTCAACACAGGTTGCCTGGAACACGATGTTGTCCATGGCGCGCCCCCGCGCCCCCGCCGCCCAGCCTAATGGGGACCAGTATGCCCTGACCACCAGAACACAACACATATGCCCTTAACACACAC   | A N Y A K G V L K R D N V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TECATTGTAGECCTTTCCAACAGCTTACGGTCATGGACATCAGTCGGCGACTCGGGTTTATATCCTTTAAGCCAAGGACATCAGTTTCGCCCCTTACAGGGCCCCCACCTTCAG  C I V G L S N K L T V M O N I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGACTACAGGGTTGAGGTGAGGACGGTTTACGACGGTGTCTGGAGACGATGTTGTGCCCGGGCCCCGGGGCCCAGGTATGGGGGACGAGTATGCCTTACAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CCTCCTCAGCTTCCCAGGCGATATTGCCATTAGGCACCTTAAGGGTTGTTGTCAGTGAGGTGCGCCACTGAGGTGAGTTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTTTAGGCAGTTGAGTTTAGGCAGTTTTAGGCAGTTGAGTTTAGGCAGTTTTAGGCAGTTTTAGGCAGTTGAGTTTAGGCAGTTTTAGGGGGAACGATTTGGGGGCAACGTAGGAGTTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTTAGGCAGTTGAGTTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGCAGTTGAGTTTAGGGGGAACGTTTTGGGGGGAACGTTTGAGGCACTGAGGGGTTTAGAGTTGAGAGTTGAGTTTTTAGGCAGTTGAGTTTTTTGGGGGGTAGGCCACTTGAGGGAACAGTTTGGGGGGGAACGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGAG   | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TECATTGTAGGCCTTTCAACAAGCTTACGGTCATGGACATGTCGGCGACTGAGGGGGTTATATACCTCATTGTAGCCAAGGAGGATCAGTTTCGCCCCTTACAAGCCCCCGCACCTTACA  241 TECATTGTAGGCCTTTCAACAAGCTTACGGTCATGGGCATCTGGGGGTTATATACCTCATTGTAGCCAAGGAGCATCAGTTTCGCCCCTTACAACCCCCCCACCTTACACGCCCCCCACCTTACA  242 L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  243 GAGATCCTGAACTACAGGGTTGAATGGCGTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCCTTGACGACCTGCGGGCGCCAGCGTAATGGGGAACTACGAGGATTACGAGGGTTAACGACGGTGTCCTGGAAGACGATGTTGGGGGCCAAGCTGATGGGGAACTACAGGATTATACGAGCAGCTTAAAGGGTGTTGTCAGTCA  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCCCACCTCGAGGTTATATCCTCGTTTAAGCCAAGGAGGACGATTTGGCCCCTTACAGCGCCCCCGAGCTTGAG C I V G L S N K L T V M D N I G D S
G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H W Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTTGCACAAGCGTGTCCTGGAAGACGATGTTGTGCCCACTGTGCCCGCGCCCGAGCGTATGGGGGACGCCAGGGTTAAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCCGCCGGATATTGCCATTAAGCGTGTTGTCAGTGAGTTCTGATGTGAGGTGAGGTTGAGGTTAGAGTTAGAGTTAGATTTACAGGCGTAATTTGAGCAGT C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  601 TTGAGGGACAACCAAGAACTCTCCTCTTACCCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGCAGTTACAACAAGTGGCCGAGGAGAGAGTTTGGGGGCAACCCAACCAA  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGCAACTGTGGCGCTCGGGGTGTTATATCCTCGTTTAAGCCCAGGGGGCCAGCTTGAGCCCCCGAGCTTGAGCCCCCGACCTTGAGCCCCCCGACCTTGAGCCCCCCGACCTTGAGCCCCCCGACCTTGAGCCCCCCGACCTTGAGCCCCCGACCTTGAGCCCCCGACCTTGAGCCCCCGACCTTGAGCCCCCGACCTTGAGCCCCCGACCTTGAGCCCCCGACCTTGAGCACGCAC  | A N Y A K G V L K R D H V H D A V R T R Y G R K L W P P D T E G R V A G R L K L  241 TECATIGIAGGCCTITICCAACAGCTTCACGTCATEGCACTICGCGCACCTTGAG C I V G L S N K L I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGCGTCTTGAGGTCCTGGAAGAGGAGGTGTTGTGCCCCTGGGGGCCCAGCGTATGGGGGACECCAGGGTTGAGCCCTGGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGCGGATTTGCGATAGGGGGTTGTGTGTG   | A N Y A K G V L K R D H V H D A V R T R Y G R K L W P P D T E G R V A G R L K L  241 TECATIGIAGGCCTITICCAACAGCTTCACGTCATEGCACTICGCGCACCTTGAG C I V G L S N K L I V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGCGTCTTGAGGTCCTGGAAGAGGAGGTGTTGTGCCCCTGGGGGCCCAGCGTATGGGGGACECCAGGGTTGAGCCCTGGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGCGGATTTGCGATAGGGGGTTGTGTGTG   | A N Y A K & V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGCTCATGGCGACTCGGGGTTATATCCTGTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGCCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCCCGCGGCCCCGCGGCCCAGCGTAATGGGGGACGCCAGGTTAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCCATAAGGCAGCTTTAAGGTTGCAGTGAGTCTGATGTGAGTGA  | A N Y A K & V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGCTCATGGCGACTCGGGGTTATATCCTGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGCGGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCCCGCGGCCCCGCGGCCCAGCGTAATGGGGGACGCCAGGTTAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCCATAAGGCAGCTTTAAGGTTGCAGTGAGTCTGATGTGGGGGATCGACTGATGAGTTGAGGTTGAGTTTATCAGCCATAGTTTTGAGCAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGAGCCCTCATGAGCCCCCCCC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGCTATGACCATGGCGACTCGGGGTTATATCCTGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480 GAGATCCTGAACTACAGGGTTGAGATGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGCCCGGGCCCCCGCGGCCCCAGCGTAATGGGGAAGCCCAGGTTACGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGCGCGCATATTGCCATTAGGCCACCTTAAGGGTTCTCAGTGAGTCTGATGTAGGCAATGCCGCACTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGATAACCAGAAGATGCCCTCCAGGGGGGTACCCCCCAGGGGGGTACCCCCCAGGGGGTAACCTCCCAGGGGGTACCCCCCAGGGGGTACCCCCCAGGGGGTACCCCCCAGGGGGTAACCAGAAGATGACAAAGATGGCCAGGAGAGACGTTTGCCCTTCAGGGGAACACCCCTCCAGGGGGTACCCCCCAGGGGGTAACCACAAGATGAGATACAACAAGATGGCCAGGACAACCAGCCCTC L R D N Q K I L L Y A V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L  721 ACCCAGAGAGGACCTTTCCCAGCTCCTAAGGAGGTCCTCTTAGGGCTAACCTTAGGGGCAACTTTCCCTGGAGGCCGTTTAACTGCCTTTCCTTCTTTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCTAGGGCCCATTAGGGGCCCCTTTTTTCCCTTTTTTTCCCTTTTTTTT | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGGCTTAGGCATGTGGCGACTCGGCGGTTATATCCTCTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  480  480  480  480  480  480  481 CTCCTCAGCTTGCGCGCGCGATATTGCCATAAGCACGTTCTCTGGAAGACGATGTTTGCCGCGCTCCGCGGCCCAGCGTAATGGGGAAGCGCAAGTATTGCCATTAGCACTCCTGAGGGGTTCCTCAGGGGGTACCCCCAGCGTTAAGGGTTGAGGAG  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGGCTTAGGCATGTGGCGACTCGGCGGTTATATCCTCTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  480
GAGATCCTGAACTACGAGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGCCCGGCCCCCAGCGTAATGGGGACGCCAGGTTAACGACGAGGAGACGATGTTGCCCTTGACGACGAGGAGACGATGTTGCCCTTGACGACGACGATGTTCCCTTGACGACGAGGAGACGATGTTGCCCTTGACGACGACGAGGTTAACGACGAGGTGTTAACGACGAGGTGTTCAAGGAGAAGACGATGTTGCCCTTGACGACGACGATATTACCAACGAGTTTAACGACGACGATTTCCAGTCAAGGAGTTCTAAAGGTTGATGTAAGGATGAACAACAAGATGGTTGAGGTTGAGGTTAACGACCACAGGTTTAACGACGCTCCAAGGGTGTTCAAGGATATAAAGGATGACAACAAGATGGTCGAAGACACAACAAGATGGCCAAGGTTTGCCCTTGACGACACCTCCAAGGGGTGATCACCTCCAAGGGGTACCCCCCAAGGAGAACAACAAAGATGGCCAAGAACAACAAGATGACCACAAGAACACCCCTCCAAGGGGAACACCCCCCCAAGGGAACAACAAAGATGACAACAAGATGACCAAGAACACACCCCTCCAAGGGGGAACACCCCCCCAAGGGAACAACAAAGATGACAACAAGATGGCCAAGACCACCCCCCCAAGGAACACCCCCCCAAGGAACAAC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTGGCCTTTCCAACAGCTTGAGCACTGGCCACTTGAGCCACTCGGGGTTATATCCTGTTTAAGCCAAGGAGCATCAGTTTGCCCCCTTACAGCCCCCCACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  480 GAGATCCTGAACTACCAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTGTGCCCGGGCCCTCCGGGCCCAGCGTAATGGGGGACGCCAGGTTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCACCTTGCGCGCGCGATATTGCCATAAGGCAGCTTTAACGGTTGTTGCTCAGTGAGTTGTGAGGTTGAGTTGAGGTTGAGTTTACAGCCAGTTTATGACGAC L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  482 Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTGAGCCTCCAGGGGGGTACCCCCCATGGAGATATATGAGATTACAACAAGATGGCCAGGTTGAGCGCACTTCCTTGAGCGTTACCTCTCAGGGGGTACCCCCCATGGAGATATTATGAGAGTCAACAAGATGGCCAGGAGGAACAGCCCTTC L R D N Q K I L L Y A V M T S Q G G T P T E E Y R K Y N K M A E E Q F G G N A L  721 ACCCAAGAGAGCCTTCCCAGCGCACTTGAACCTTGTGAGCTTGTCGCACATTCAGGGGCCACTTTTTCCCTGTTAACGTTTACCTCCTAGGGGCAACTCTTCTTTCCTTTTTCCTTTTTCCTTTTTTCCTTTTTCCTTTT | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGGCTTAGGCATGTGGCGACTCGGCGGTTATATCCTCTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  480 GAGATCCTGAACTACGAGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGCCCGGCCCCCAGCGTAATGGGGACGCCAGGTTAACGACGAGGAGACGATGTTGCCCTTGACGACGAGGAGACGATGTTGCCCTTGACGACGACGATGTTCCCTTGACGACGAGGAGACGATGTTGCCCTTGACGACGACGAGGTTAACGACGAGGTGTTAACGACGAGGTGTTCAAGGAGAAGACGATGTTGCCCTTGACGACGACGATATTACCAACGAGTTTAACGACGACGATTTCCAGTCAAGGAGTTCTAAAGGTTGATGTAAGGATGAACAACAAGATGGTTGAGGTTGAGGTTAACGACCACAGGTTTAACGACGCTCCAAGGGTGTTCAAGGATATAAAGGATGACAACAAGATGGTCGAAGACACAACAAGATGGCCAAGGTTTGCCCTTGACGACACCTCCAAGGGGTGATCACCTCCAAGGGGTACCCCCCAAGGAGAACAACAAAGATGGCCAAGAACAACAAGATGACCACAAGAACACCCCTCCAAGGGGAACACCCCCCCAAGGGAACAACAAAGATGACAACAAGATGACCAAGAACACACCCCTCCAAGGGGGAACACCCCCCCAAGGGAACAACAAAGATGACAACAAGATGGCCAAGACCACCCCCCCAAGGAACACCCCCCCAAGGAACAAC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGCTATGACCATGGCGACTCGGGGTTATATCCTGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  480 GAGATCCTGAACTACAGGGTTGAGATGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGCCCGGGCCCCCGCGGCCCCAGCGTAATGGGGAAGCCCAGGTTACGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGCGCGCATATTGCCATTAGGCCACCTTAAGGGTTCTCAGTGAGTCTGATGTAGGCAATGCCGCACTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGATAACCAGAAGATGCCCTCCAGGGGGGTACCCCCCAGGGGGGTACCCCCCAGGGGGTAACCTCCCAGGGGGTACCCCCCAGGGGGTACCCCCCAGGGGGTACCCCCCAGGGGGTAACCAGAAGATGACAAAGATGGCCAGGAGAGACGTTTGCCCTTCAGGGGAACACCCCTCCAGGGGGTACCCCCCAGGGGGTAACCACAAGATGAGATACAACAAGATGGCCAGGACAACCAGCCCTC L R D N Q K I L L Y A V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L  721 ACCCAGAGAGGACCTTTCCCAGCTCCTAAGGAGGTCCTCTTAGGGCTAACCTTAGGGGCAACTTTCCCTGGAGGCCGTTTAACTGCCTTTCCTTCTTTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCTAGGGCCCATTAGGGGCCCCTTTTTTCCCTTTTTTTCCCTTTTTTTT | A N Y A K & V L K R D H V H D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 TOCATTGTAGGCCTTTCCAACAAGCTTAGGCTATGGCGACTGGGGGTTATATCCTGTTTAAGCCAAGGAGGATCAGTTTGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  361 GAGATCTGAACTACAGGGTTGAGATGCCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCCGCGCCCCCAGCGTAATGGGGAACGCCAGGTTACGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGCGCGATATTGCCATAAGGCAGCTTTAAGGGTTGTCTAGTGAGTCTGAGTGTGAGTTGAGGTTGAGGTTGAGTTTATCAGGCGATATTATCAGGCGATATTATCAGGCAAGTTCTCAGTGAGTCTCAGTGAGTCTCTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTAGAGGTTGAGGTTGAGGTTAGAGGTTGAGGTTAGAGGTTGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGTTAGAGGAACACCAGAAGATCCTCCCAGGGGGGTAACCCCCCAGGGGGGTAACCTCCCAGGGGGGTAACCAGAAGATCCACAAGAAGATCCTCCTAGAGCTCCCAGGGGGGTACCCCCCACTGAGAATTATAGGAAGATACAACAAGATGGCCAGGAACCTCCCTAGAGCCCCTCTAAGGGGTACCCCCCACTGAGAATTATAGGAAGTACAACAAGATGCCAGGAACCTCCCTAGAGCCCCTCTAAGGGGTACCCCCCACTGAGAACTACACAAGAAGATCCTCCCAAGGAACTTCCCCTAGAGCCCTTTAAGCCTCTCAAGGGGGTACCCCCCCACTGAGAACTTCCCCTAGGGGGAACACCACACACA  | A N Y A K G V L K R D H V H D A V R T N Y G R K L W P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAGCAAGCTTAGGGTCATGGACGACTGGGGTGTTATATCCTTCATGAGCACGGATCAGTTTGGCCCCCTAACAGCCCCCCCC  
  | A N Y A K G V L K R D N V N D A V R T N Y G R K L N P P D T E G R V A G R L K L  241 T9CATTGTAGGCCTTTCCAACAAGCTTACGGTCATEGACCATGACCGCCCCACTGGATTATACCTTCATTTAGCCAAGCAGCACCTTAAGCCCCCCCC  | A N Y A K & V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGCCACTCGGGTGTTATATCCTTCAGGCCAAGAGAGCAGTTTCGCCCCCTAACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGACTCTGAACTACAGGGTTCAAGAGCGTTCAGGCAAGAGCAGTTCTGGCCGGCC   | A N Y A K & V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGCCACTCGGGTGTTATATCCTTCAGGCCAAGAGAGCAGTTTCGCCCCCTAACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGACTCTGAACTACAGGGTTCAAGAGCGTTCAGGCAAGAGCAGTTCTGGCCGGCC   | A N Y A K & V L K R D H V H D A V R T N Y G R K L H P P D T E G R V A G R L K L  241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGCCACTCGGGTGTTATATCCTTCAGGCCAAGAGAGCAGTTTCGCCCCCTAACAGCGCCCCGCAGCTTGAG C I V G L S N K L T V N O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  460 GAGACTCTGAACTACAGGGTTCAAGAGCGTTCAGGCAAGAGCAGTTCTGGCCGGCC   | A N Y A K G V L K R D H V H D A V R T N Y G R K L M P P D T E G R V A G R L K L  241 TGCATTGTGGCCTTTCCAACAGCTTAGGGTCATGGGCCATGTGGCCGCCTCGGGGTGTATATCCTCGTTTAGCCCAGGAGCATCAGTTTCCCCCTTACAGCGCCCCGCAGCTTGAG  26 C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  26 C G V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  26 C G V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  27 C G V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  28 C G V I V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  29 C L L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  20 C C C C C C C C C C C C C C C C C C C  |
| TECATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTCGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTAACAGCGCCCCGCAGCTTCCCCCCCAACTACCACCACCACCACCACCCCCAACTACCACC  | CATEGACATGATCGGCGACTCGGGTGTTATATCCTCGTTTAAGCCAAGAGGATCAGTTTCGCCCCTTACAGCGCCCCGCAGCTTGAG  M O M I G O S G V I S S F K P R R I S F A P Y S A P Q L E  V Y T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  TAACGACGGTGTCCTGGAAGACGATGTTGTGCCCACTGTGCGCGGCCCCGCGGCCCAGCGTAATGGGGGACGCCAGGTATGCCCTTGAC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GCACCTTAAGGGTGTTCCAGTGGAGTCTGATGTGAGGATGGGGACGACTGAGAGGTTGAGGTTTAACGGCTAGTTTATCAGGCGTAGTTTAGAGAGA  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  CGTCATGACCTCCCAGGGGGGACTCCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGGGCAACGCCCCTC  V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCGAGGGGCCCGTGGGAGGGGGGTTAACTGGCCTTGTTCCTTCTCCTCT  L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D •  GAGGTCCCCTTGAGGGCTAACCTAGGGGCAACTTTCTCTTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCCATAGTTTTT  P60  CACCCCCATTTTTCCCTTATTTGCCAGAGCCAACTTTCTCTTGGATTTTTTGCCTGTTAGTGAACTCCCCTATTTTTTTATGACCTCCATAGTTTTTT  P60  TACTTCACAAAAGAGTGGTTGATATTACAGGCTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTTT  P60  TACTTCACAAAAAGAGTGGTTGATATTACAGGCTTCTATATTACTTATATAGGATGACTGTTACAGTATCTTTTACTCAAGGGTGTTTTTT  P60  CACCGCCCATTTTTCCCTTATTTTCCCAGAGCAACTTTTTTTCCTTGGTTTGTTT  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCACTGACCGGCGCTCGGGCTTGATATCCTCGTTTAAGCCAAGGACCAGTTTCCCCCCTTACAGCGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCACCCGTGACACAGATCCTGACACAGGCAGTCTCTGCCAACACAGGATCCTGACACAGGCGTTCACAGGGTTGCCCCCTGACACAGGGTTCTGCCCAGCTTGCGGGGCCCCAGCGTAAGGCGTAAGGCGTTACAGGGGGTCCCCGGGGCCCAGCGTCGCGGGCCCCAGCGTAAGGCGTAAGGCGTTACAGGCAGCTTGAGGCAGCTCTGAGGAAGACGAGTTTGTGCCACCTCGGGGGCCCCAGCGTAAGGCGTAAGGCGTAAGCCGTTGAGGAGCCCCCAGCTTGAGGAGATCCAGAGATCCTCACAGGGGAACAGCACCCCCAACGAGATCCCCCAACAGAAGATCCCCCAACAGAAGATCCCCCAACAGAAGATCCCCCCAACAGAAGATCCCCCCAACAGAAGATCCCCCCACCGGGGGGGAACACCCCCAACGAGATCCCCCCAACGAGAACACAAGAAGATCCCCCCTGAAGAGATCCCCCCACTGAGGATATTGAGGCAACAAGAAGATGGCAACAAGAAGATGCCCCCCCACGGGGGGAACACCCCCACCTGAAGAGATACAACAAGAAGATGGCAACAAGAAGATGCCCCCCCACCGGGGGGGAACCCCCCACCTGAGGATATTAAGGAATAAAGAAGAAGAAGAAGAAGAAGA  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGCGGCGACCTGGGGCACCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTAATGCCCCCTTAAAGGCGCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCATCCCTGAAAGCAGGCATTAAAGGAGAACATTTAAAGGCAGCCCCCAGGCCCAGCCCAGCCCCAGGCCCAGCCCAGCGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCCAGCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCAGCCCCCAGCCCCCAGCCCCCC  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGTGGGCGACTCGGGGTGTTATATCCTCGTTTAAGCCAAGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P Y G P I G K V GAGATCCTGAACTACAGGGTTGACGTGCGCTTTAACGAGGGTGTGTGT   | 241
TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGTGGGCACTCGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R R R L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTACCAGGGGTGTCCTGAAGGAGGTTGTGCCACTGTGCCGGGGCCCAGGGCGCAGGGGGAGCAGATGGGGAACCCTGAACTACAGGGTTGAAGGCAGTTTAAGGAGAGTGTTGTCCAGTGGGGAGGGGTGGGCGCGGGCCCAGGGGGGAGAGCCCCTGAAGGAGCCCTGAAGGAGCAGTTAGAGGTGTTGTCAGTTGAGTTGAAGTTGAGCTGCAGGGGGCCAGCGGGCCAGGGGGGAGAACTAGAGGGTATGCGGATAGGGCAACTAAGGGGGTTGTCAAGTTGAGTTGAAGTTGAAGTTGAAGTTGAGCTTGAAGTTGAAGTTGAAGTTGAAGTTAGAAGAGATGAAGATTAGAGAAGA   | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGTGGGCACTCGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R R R L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTACCAGGGGTGTCCTGAAGGAGGTTGTGCCACTGTGCCGGGGCCCAGGGCGCAGGGGGAGCAGATGGGGAACCCTGAACTACAGGGTTGAAGGCAGTTTAAGGAGAGTGTTGTCCAGTGGGGAGGGGTGGGCGCGGGCCCAGGGGGGAGAGCCCCTGAAGGAGCCCTGAAGGAGCAGTTAGAGGTGTTGTCAGTTGAGTTGAAGTTGAGCTGCAGGGGGCCAGCGGGCCAGGGGGGAGAACTAGAGGGTATGCGGATAGGGCAACTAAGGGGGTTGTCAAGTTGAGTTGAAGTTGAAGTTGAAGTTGAGCTTGAAGTTGAAGTTGAAGTTGAAGTTAGAAGAGATGAAGATTAGAGAAGA   | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGTGGGCACTCGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R R R L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTACCAGGGGTGTCCTGAAGGAGGTTGTGCCACTGTGCCGGGGCCCAGGGCGCAGGGGGAGCAGATGGGGAACCCTGAACTACAGGGTTGAAGGCAGTTTAAGGAGAGTGTTGTCCAGTGGGGAGGGGTGGGCGCGGGCCCAGGGGGGAGAGCCCCTGAAGGAGCCCTGAAGGAGCAGTTAGAGGTGTTGTCAGTTGAGTTGAAGTTGAGCTGCAGGGGGCCAGCGGGCCAGGGGGGAGAACTAGAGGGTATGCGGATAGGGCAACTAAGGGGGTTGTCAAGTTGAGTTGAAGTTGAAGTTGAAGTTGAGCTTGAAGTTGAAGTTGAAGTTGAAGTTAGAAGAGATGAAGATTAGAGAAGA   | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATGGGCATGTGGGCACTCGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTACGCAGGGTGTCCTGGAAGGAGGTTGTGCCACTGTGCGCGGGCCCAGGGCCCAGGGGGAGCAGATCAGGGATAGGCCATTACACGGTTAACGCCCTCAGGAGAGAGA  
   | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCTATGAGCAGTGCGGCGACTTGAGGCGCCCCAACTTGAGGCCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCAACCAAC  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCTATGAGCAGTGCGGCGACTTGAGGCGCCCCAACTTGAGGCCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCAACCAAC  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT   
  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCATTGGGCAACTTGGGCGACTTGGGCACCTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCATCCCCAACTTGAGGCATCCCCAACTCCAACTACAACGGCCTTAACAACGGCCTTGAACTAGAGGATCCTCCAACTACAACGGCCTTAACAACGGCCTCAACGAACTCCTCAACTAACGAACACTTGAACTAACT  | 241 TSCATIGIAGECCITICCAACAGCITIACGGTCATEGGACATGGACCGCCACTGCAGCCTCCGGTGTTATATCCTCGTTTATAGCCAAGGAGGACCAGTTCCCCCTTACAGGCCCCGCAGCCTTGGAGCCCCCCCAGCCTTGAGCCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGCACTGGGCACTCGGGGTTATATGCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGGCCCCGCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  AGAGATCCTGAACTGACGGTTGAGATGGCGTTTAAGCGCTTGGAGAGGAGGATGTTGTGGCCCTTGGCCGGGCCCGGGGCCTGAGGGGGACCCCGCGTTGACCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGGGGCGATATTGCCATTAGGCACTTAAGGTGTTGTGTGAGGATGGGGACTGAATGGGGACTGATGTTAAGCATGGGGACTGAATGGGGACTGATGTTAAGCAGGGGACTGATGTTAAGCAGGGGACTGAAGGAGGATGTTTAAGCAGGGGGACTGAAGGAGATGAGGTTTAAGCAGGGGGACTGAAGGAGAGGATTAAGGGATTATTGAGCAGGGGGACTGAAGGAGAGATGAGGGGACTGAAGGAGAGATGAGGGGACTGAAGGAGATGAGAGTTGAAGATGGGGGACTGAAGAGATGGGGGACTGAAGAGATGAGAGAGA  
   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGCACTGGGCACTCGGGTTATATICCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGGCCCCGCAGCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAAGGCGTTCTCTGGAAGAGGAGTTGTGCCCTTGGCCGGGCCCGGGGCCCGGGCCTAATGGGGACCAGCTTGACCACTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGGGCGCATATTGCCATAAGGCACTTAAGGCTGTTCTGTGAGGATGGGCGACTGATGGGGCCTGAGGTTAGGGGTATATTGAGCAGG C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  601 TTGAGGGACAACCAGAAGATCCTCTCTGCGCGTCTCATGGGGGGGTCCCCCACTGGAGGTTATATAGGAAGTGGCCGAAGAGTGGGGGAACTTCTCTCTTGGGGGGCAAGCCCCCCCC   | 241 TSCATIGIAGECCITICCAACAGCITIACGGTCATEGGACATGGACCGCCACTGCAGCCTCCGGTGTTATATCCTCGTTTATAGCCAAGGAGGACCAGTTCCCCCTTACAGGCCCCGCAGCCTTGGAGCCCCCCCAGCCTTGAGCCCCCCCC  | 241 TGCATTGTAGGCCTTTACCACAAGCTTACGGTCATGACTGAC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGCACTGGGCACTCGGGTTATATICCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGGCCCCGCAGCTTGAG C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAAGGCGTTCTCTGGAAGAGGAGTTGTGCCCTTGGCCGGGCCCGGGGCCCGGGCCTAATGGGGACCAGCTTGACCACTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGGGCGCATATTGCCATAAGGCACTTAAGGCTGTTCTGTGAGGATGGGCGACTGATGGGGCCTGAGGTTAGGGGTATATTGAGCAGG C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  601 TTGAGGGACAACCAGAAGATCCTCTCTGCGCGTCTCATGGGGGGGTCCCCCACTGGAGGTTATATAGGAAGTGGCCGAAGAGTGGGGGAACTTCTCTCTTGGGGGGCAAGCCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGCACTGGGCACTCGGGTGTTATATCTTCTTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGGCCCCGCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTGAAGGGTTGAGATGGCGTTTAAGCGCTTGGAGAGAGGATGTTGTGGCCCTTGGCCGGGCCCGGGGCCTGAGGGGGACCCCGCGTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGCGGCGATATTGCCATTAGGCACTTAAGGTGTTGTGTGAGGATGGGGACTGATGGGGACTGATGGGGACTTATTGAGCTAGGGGACTCCCAAGGTTGTTGAGCATGGGGACTGATGGGGACTGATGGGGACTGATGTTGAGCATGGGGACTGATGTTGAGCATGGGGACTGAAGGATGAGGTTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGAGATGAGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAGAGATGAGAGAGAGAGATGA   
   | 241 TGCATTGTAGGCCTTTCCAACAGCTTAGGGCTATGAGCAGTGCGGCGACTTGAGGCGCCCCAACTTGAGGCCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCCCCCAACTTGAGGCAACCAAC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGCCCAGGGGACCCAGGACCCCCTTAACCAGGGTTCCTCTGAAGAGAGATGTTGCCCCTGCAGCCCCAGGCCCAGGGGCCCAGGGGACCCCCCCC  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGCCCAGGGGACCCAGGACCCCCTTAACCAGGGTTCCTCTGAAGAGAGATGTTGCCCCTGCAGCCCCAGGCCCAGGGGCCCAGGGGACCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGCCCAGGGGACCCAGGACCCCCTTAACCAGGGTTCCTCTGAAGAGAGATGTTGCCCCTGCAGCCCCAGGCCCAGGGGCCCAGGGGACCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGCCCAGGGGACCCAGGACCCCCTTAACCAGGGTTCCTCTGAAGAGAGATGTTGCCCCTGCAGCCCCAGGCCCAGGGGCCCAGGGGACCCCCCCC   | 241
TGCATIGTAGGCCTTTCCAACAAGCTTAGGGCTATGGCAATCAGCGGCACTTGAGGTTTATACCTTCAAGCGCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCAAGCAA   | 241 TGCATIGTAGGCCTTTCCAACAAGCTTAGGGCTATGGCAATCAGCGGCACTTGAGGTTTATACCTTCAAGCGCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCAAGCAA   | 241 TGCATIGTAGGCCTTTCCAACAAGCTTAGGGCATGTGGCGACTGGGCGTGTTATATCCTCGTTTAAGCCAAGGAGCATCAGTTTCCCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACCACGGGTGTCCTGAAGAAGAGAAGTTTGTCCCCTGTGTGAAGTACACAGGGTTGTTAACCACGGTTCTCTGAAGAAGAGAAGAGAAGAAGAGAAGAAGAAGAAGAAGAA  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCATGTGGCGATCTGGGCGTGTTATATCTTCGTTTAAGCCAAGGAGGATCAGTTTGCCCCTTAAGGCGCCCCGCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H M Q A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAAGTGCGTTTAACGAGGGTGTCCTGGAAGAAGAAGAAGATGCTGCCCTGGCAGCCTGCGGCCCGCGGGTGTATGGGACCCTAGGTATGCCCTTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGCGGATATTGCGATAAGGCAGCTTCTAGGTGTGTGCTGATGTGAGTTGAGGTGCGACTGATGAGGTTTAGGTTTAGGTAGG  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCATTGAGCTCGGCGATCTGGGGCTTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTAAAGCGCCCCGCAGCTTGAG C I V G L S N K L T V M O N I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N D A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAACTAGGGGTTAACGAGGGTGTCCTGGAAGAACGATGTTGTGCCCCTGGAGCCTCGGGCCTGCGGGAGCCTGAGGAACCCCAGGGTAGCCCTTAACCACGGGTTTCCCTGAAGAACGAAGAGAGAACATTCAGAGGTTGAGTTAACAACAAGAGTGCCTTAACCACGGGTTCTCTGAGAGAACACAAGAACACAACAAGAACACAAAAACAACAA  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCATTGAGCTCGGCGATCTGGGGCTTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTAAAGCGCCCCGCAGCTTGAG C I V G L S N K L T V M O N I G O S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N D A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAACTAGGGGTTAACGAGGGTGTCCTGGAAGAACGATGTTGTGCCCCTGGAGCCTCGGGCCTGCGGGAGCCTGAGGAACCCCAGGGTAGCCCTTAACCACGGGTTTCCCTGAAGAACGAAGAGAGAACATTCAGAGGTTGAGTTAACAACAAGAGTGCCTTAACCACGGGTTCTCTGAGAGAACACAAGAACACAACAAGAACACAAAAACAACAA  
   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGCCCAGGGGACCCAGGACCCCCTTAACCAGGGTTCCTCTGAAGAGAGATGTTGCCCCTGCAGCCCCAGGCCCAGGGGCCCAGGGGACCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGGACCAGGGTAGGGGAACCCCTGAACACAGGGTTGAACCAGGGTTCCCTGAAGAAGAGTGTTGTCCAGTGGGGACCCCCCCGGCCCCAGGCCCAGGGGGACCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCCCC   | 241 TGCATIGTAGGCCTTTCCAACAAGCTTAGGGCTATGGCAATCAGCGGCACTTGAGGTTTATACCTTCAAGCGCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCCCCCAAGCTTGAGGCAAGCAA   | 241 TECATTGTAGGCCTTTCCAACAAGCTTAGGCTCATGGACATGATCGGCGACTGGGGGTTATATCCTTCAAGCGCCAAGCTTTCAGCCCCCTACAGCGCCCCCAAGCTTGAG C   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGACATGATCGGCGACTTGAGG C I V G L S N K L T V H D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGCCGGTGCTCGAGAGGGTTGTGCCCCTGAAGGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGAGGGTTGAGGAG   | 241 TGCATIGTAGGCCTTTCCAACAAGCTTAGGGCATGGGCATCGGGGGCTTGAGGCCCCCAAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGACGAGGCGTTTAACCACGGTGCTCCTGAAGAGGAGAGTTGTTGGCTGCCCTGCAGCCTGGGCCCCAGGCTAAGGGGACCCCTGAGTTACCACGGTTTACCACGGTTGTCCCTGAAGAGGAGGAGGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGGACCCCGGGGTAAGGGGATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCACCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGGTGTTGTCAGTGGGTTGGGGGAGGGGGCGCACGTTGAGGTTTGAGTTTATCAGGCGTAATTGAGCAG C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  601 TTGAGGGACAACCAGAAACCCCCCTGAAGGCACCTCCAGGGGGGTACCCCCCCC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGACCAGCACTGAGGGGTTATATCCTCTTTTAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCGAGCTTGAGGCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGCCCCCAGCTTGAGGACCAGTTTCTGCCAACACAGATGCTTTAAGGACGGTTCTTGAGAACACGATGTTGTGCCAGCTTGCCCAGCGTCGCGGGCCCAGCGTATGGGGAACACCATTAAGGAGTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTCTAAGGACGATGTTGCCCCAGCGTTCAAGGATGCCATTGGGGAACACGCTTGAGGATATTGAGGACAGATGCCCCATTAAGGACTTGAGGAGATATGAGGAAGAAGAAGATGCCCCCAACTGAGGATATTGAGGACCCAAGAAGATGCCCCCAACTGAGGATATTGAGGACAGAAGAAGATGCCCCCAACTGAGGATATAAGAGAGAG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGACCTGGCGACTGGGGGTTATATCCTCGTTTAAGCCAAGGAGTCAGTTTCCCCCCTTACAGCGCCCCGAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F
A P Y S A P Q L E  L D Q V V P M L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GACATCCTCAACTACAGGGTTGACGACGGTTTCAGCACGGTGTCCTGGAAGACGAGTTGGCCCAGCGTCGGGGCCCAGGGTATAGGGGATGCCCTTTAACGACGGTGTCCTGGAAGACGAGTTGGCGAGCCGGGCCCAGGGTATAGGGATATGCCATAAGGAGTTAAGGACGTGCCCAGCGTTGAGGACGAGTGCCCAGCGTGCGGGCCCAGGGTATAGGGAATAGGCCATAGAGGTGCTGAGGTGTGAGGATGAGGGCCAGGTATTGCGATAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCCACTTAAGGCAGTTGAGGTCTGAAGGTGCCAACTGAGGTTCAAGGTGAGGTTGAGGTTGAGGGTAGAGTTTAAGGAAGTACAACAAGAGTGCCACATGAGGTTCAAGGTTGAGGGTAAGGCCAACGCCCACCCA  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTCAGGGTCATGGGCACTCGGGTGTTATATCCTCGTTTAAGCCAAGGATCAGTTTCGCCCCTTACAGCGCCCCGAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H W Q A R R E R G L T I P V G P I G K V  480  480  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R H G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  481 CTCCTCAGCTTCGCAGCGCAGTTTAAGCCACTTAAGGGTTTGTTGTGTGTTTTTGGCACTTGAGTTGGGTTGAGTTTGGGTTAATTTCAAGCTAGTTTTTTAAGCCACTTTTCGCAGCAGCAGTTTGAGTTGGGTAACTTAAGGTTGTTTTAAGGTTGTTTAAGGTTGTTTAAGGTTGTT   | 241 TGCATTGTAGGCCTTTCCAACAGCTTACGGTCATGGACATGATCGGCGACTCGGGTGTTATATCCTCGTTTAAGCCAAGGATCAGTTTCGCCCCTTACAGCGCCCCCCAGCTTGAGGCCCCCCCAGCTTGAGGCCCCCCCC  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGGGGTGTTATATCCTCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCCTTACAGCGCCCCCGACTTGAGGCCCCCGCACTTGAGCCCCCCGCACTTGAGCCCCCCCAGCTTGAGCCCCCCCAGCTTGAGCCCCCCCC  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGCTCTGGGTGTTATATCCTCTGTTTAAGCCAAGGAGCATCAGTTTCGCCCCCTTACAGCGCCCCCCAGCTTGAGCCCCCCCC  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGGCGCCCCGGGGTTATATCCTGGTTTAAGCCAAGGAGGATCAGTTTCGCCCCCTTACAGCGCCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTTGAGAGAAGATGTTGTGCCACTGTGCGCGGGCCCTGGGGCCCAGGGTAATGGGGAAGCCCTGAACGCGTTTAACGACGGTGTTCCCTTGAGAGAAGATGTTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGGGGATATGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGTGGGGAAGTCGGATGGAT  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGACATGGCGCCGCCGGGTTATATCCTGGTTTAAGCCAAGGAGGATCAGTTTCGCCCCCTTACAGCGCCCCCCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTTGAGAGAAGATGTTGTGCCACTGTGCGCGGGCCCTGGGGCCCAGGGTAATGGGGAAGCCCTGAACGCGTTTAACGACGGTGTTCCCTTGAGAGAAGATGTTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGGGGATATGCGATAAGGAGGTTGTGTGTG  | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTTATATCCTCGTTTAAGCCAAGGAGTACAGTTTCGCCCCCTAACGCCCCCCGCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V 
361 GAGATCCTCAACTACAGGGTTGAGATGGCGTTTAACGACGGTSTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGGCTCGGGGCTCAAGGGTAATGGGGAACGCCATTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGGGATATGGCGATAAGGCAGCTTAAGGTGTTGAGTGAG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTTATATCCTCGTTTAAGCCAAGGAGTACAGTTTCGCCCCCTAACGCCCCCCGCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTTGAGATGGCGTTTAACGACGGTSTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGGCTCGGGGCTCAAGGGTAATGGGGAACGCCATTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGGGATATGGCGATAAGGCAGCTTAAGGTGTTGAGTGAG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGTCATGGACATGATCGGCGACTTGGGTGTTATATCCTCGTTTAAGCCAAGGAGTCAGTTTCGCCCCCTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M 0 M I G 0 S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTGAAGTGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTTGTGGGGGGCGCGCTGGGGGCCTGGGGGCTCAAGTGGGGAAGGCCCAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGAATATGCGATAAGGAGGTTGTTGCAGTGAGTG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTGTTATATCCTCGTTTAAGCCAAGGAGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTTGTGCGGGGCGCTCGGGGCGCTCGGGGGCGCCCAGGGTAATGGGGGACGCCAGGTTAATGGCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGCATATGCGATAAGGGCGTTTAAGGATGTTGAGTGCAGTGAGGGGGGGG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTGTTATATCCTCGTTTAAGCCAAGGAGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTTGTGCGGGGCGCTCGGGGCGCTCGGGGGCGCCCAGGGTAATGGGGGACGCCAGGTTAATGGCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGCATATGCGATAAGGGCGTTTAAGGATGTTGAGTGCAGTGAGGGGGGGG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCAATGAGCGGCCACTGGGGTGTTATATCCTCGTTTAAGCCAAGAGGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTGTGCGGGGCGCTCGGGGGCCCCAGGGTAATGGGGGACGCCAGGTTAACGACGGTTAACGACGGTGTTAACGACGGTGTTATACGACGGTGTTATACGACGGTGTAATGGGGGCCTCGGGGCGCCTCGGGGCGCCTCGGGGCCCCAGGGTAATGGGGGACGCCAAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGACGACTTAAGGATGTTGAGTCTGATGGAGGTGAGGGGGGGG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTGTTATATCCTCGTTTAAGCCAAGGAGATCAGTTTCGCCCCTTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTTGTGCGGGGCGCTCGGGGCGCTCGGGGGCGCCCAGGGTAATGGGGGACGCCAGGTTAATGGCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGCATATGCGATAAGGGCGTTTAAGGATGTTGAGTGCAGTGAGGGGGGGG   
   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGTCATGGACATGATCGGCGACTTGGGTGTTATATCCTCGTTTAAGCCAAGGAGTCAGTTTCGCCCCCTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M 0 M I G 0 S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTGAAGTGGCGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCCTTGTGGGGGGCGCGCTGGGGGCCTGGGGGCTCAAGTGGGGAAGGCCCAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGAATATGCGATAAGGAGGTTGTTGCAGTGAGTG   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTACGGTCATGGACATGATCGGCGACTTGAGGTTATATCCTCGTTTAAGCCAAGGAGTCAGTTTCGCCCCCTTACAGCGCCCCCGCAGCTTGAG C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTTGAGATGGCGTTTAACGACGGTSTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGCGCTCGGGGCTCAAGGGGTAATGGGGAACGCCTTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGGGATATGGCGATAAGGGCGCTTTGAGTGTGTGT   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGCATGGCGACTTGAGCGCGCGC   | 241 TGCATTGTAGGCCTTTCCAACAAGCTTAGGGTCATGGGGATCGGGTGTTATATCT.TCGTTTAAGCCAAGGAGGATCAGTTTCGCCCCTTACAGCGCCCCCAACCTTGAG C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAAGGCGGTTTAACCAGGGTGTCCTGAAGAGGATGTTGTCCACTGTGCGCGGCCCCAGGCCCAGGGGGACCAGGGTAGGGGAACCCCTGAACACAGGGTTGAACCAGGGTTCCCTGAAGAAGAGTGTTGTCCAGTGGGGACCCCCCCGGCCCCAGGCCCAGGGGGACCAGCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCCAGCCAGCCCCCC   | 241 TGCATTGTAGGCCTTTACCACAAGCTTACGGTCATGACTGAC   | 241 TGCATTGTAGGCCTTTACCACAAGCTTACGGTCATGACTGAC   | 241 TGCATTGTAGGCCTTTACCACAAGCTTACGGTCATGACTGAC   
   | TAGGET TO CALL TO MOUNT OF VINHUNG ARREST A PYSAPOLE  10 Q V V P N L H R K V V T D Q F V I N H N Q A R R E R L T I P V G P I G K V R I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D R L L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D R R L T CHCCLAGE CONTINUES CONTINUE |
| C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K  361 GACATCCTGAACTACAGGGTTGAGCTACCACGGTGTCCTGGAAGACCATGTTGTGCCACTGTGCGCGGGCTCGAGCGTAATGGGGACGAGTTAACCACGGTGTCCTGGAAGACCATGTTGTGCCACTGTGCGCGGGCTCGAGCGTAATGGGGACGCCAGGTTAACCACGGTTTAACCACGGTGTCCTGGAAGACCATGTTGTGCCACTGTGCGCGGGCCCAGCGTAATGGGGACGCAGTATATGGGGACGTCTGAGGTTGAGGAG  | W V T D Q F V I N H W Q A R R E R G L T I P V G P I G K V TAACGACGGTGCTCTGGAGAGAGGATGTTGTGCCCTGTGCGCGCCCCAGCGTAATGGGGGACGCCAGTTATGCCCTTGAC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I N P H R S I L N L N L K D P T T N L L GCACCTTAAAGGTTGTTGTCAGTGAGTCTTGATGTGAGCAGTGCCGACTGATGAGGTTGAGGTTGATGTTGAGCAG  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E CSTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGACTAACCAAGATTGGGGGCAACGCCCTC  V M T S Q G G I P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M ORF8: ACTTGAACTCTATGGCCTTGTCGAGATTCAGGTTGTCGCGAGGGGCCGTGGGGGGGG  | C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGCGGTTTAACGACGGTGTCCTGGAAGAGGATGTTGTGCCCACTGTGCGCGGCCCCAGGGTAATGGGGGACCCCAGGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGGCTTGCGGGCGATATTGCGATAGGGGGTTTAAGGGTTTTGTGGTTGTGTGTG   | CIVGLSNKLTVMONIGOS GVISSFKPRRISFAPYSAPQLE  LDQVVPPNLHRKVVTDQFVINHHQARRERGLTTGGGGGGGGCGCGGGGGCGGGGGGGGGGGGGGGGGG   | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATIC TGACATACAGGGTTGAGATGCGGTTTACGACGGGTGTCCTGGAAGACGATGTTGGGCGGGGCTGGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGGG   | C I V G L S
N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTTCCTGGAAGAGCATGTTGTGCCCATGTGCGCGGCCCAGGGCCAGGGGAATGGGGGAAGAGCAGTTAGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTGCAGTGAGGTGGGGGTGGGGGAGGGGTGAGGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTGAGGTGAGGTGAGGTTGAGGTTAGGGTTATTGAGCAG  L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGTTAGGGGGCAACCCCCATGAGATTTGAGCAG  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M M F E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M W V P S S S  Element D  10 P D L N L E A I R R S L *  Element D  117AGTTGGCCTGACCTCATGCTTGAGGCCATTTAGGGGTGACCCCCATTTTTCCTGGGGTTTTTTTGCCTGTTTTTTTGCTGTTGTT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTTCCTGGAAGAGCATGTTGTGCCCATGTGCGCGGCCCAGGGCCAGGGGAATGGGGGAAGAGCAGTTAGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTGCAGTGAGGTGGGGGTGGGGGAGGGGTGAGGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTGAGGTGAGGTGAGGTTGAGGTTAGGGTTATTGAGCAG  L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGTTAGGGGGCAACCCCCATGAGATTTGAGCAG  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M M F E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M W V P S S S  Element D  10 P D L N L E A I R R S L *  Element D  117AGTTGGCCTGACCTCATGCTTGAGGCCATTTAGGGGTGACCCCCATTTTTCCTGGGGTTTTTTTGCCTGTTTTTTTGCTGTTGTT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTTCCTGGAAGAGCATGTTGTGCCCATGTGCGCGGCCCAGGGCCAGGGGAATGGGGGAAGAGCAGTTAGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTGCAGTGAGGTGGGGGTGGGGGAGGGGTGAGGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTTGAGGTGAGGTGAGGTGAGGTGAGGTTGAGGTTAGGGTTATTGAGCAG  L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGTTAGGGGGCAACCCCCATGAGATTTGAGCAG  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M M F E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N M W V P S S S  Element D  10 P D L N L E A I R R S L *  Element D  117AGTTGGCCTGACCTCATGCTTGAGGCCATTTAGGGGTGACCCCCATTTTTCCTGGGGTTTTTTTGCCTGTTTTTTTGCTGTTGTT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTTCCTGGAAGAGCATGTTGTGCCCATGTGCGCGGCCCAGGGCCAGGGGAATGGGGGAAGAGCAGTTAGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGAATTGCGCTAAAGGCAGCTTAAAGGGTGTTGTGCAGTGAGGTGGAGTGAGGGGGAGTGAGGTGAGGTTGAGGTTAGAGTTAGGCAGTTAAGGCAGCTTAAGGCAGCTTAAAGGGTGTTGTCAGTGAGCTGTGAGGTGAGGTGAGGAGTGAGGAGTTAAGAGGTGTTAGAGCAG  L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGTTAGGGGGCAACCCCCAT  L R D N Q K I L L Y A V M T S Q G G T P T E E Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GFFI  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGGGCTTTGTGGCTTGTGCAGTTGTGGGCTGGCAGGGGGGGG   
   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGGCGCGCGC   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT  
  | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGGCGCGCGC   
   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGCGCGGCCCAGGGGCCAGGGGATGGGGGACAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L K D P T T N L L  CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGT   | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQRKVVTTDQFVINHHQARRERGELTGETGETGEGGGGCCTGGGGGCTGAGGGGGAGGGTATGGGGGAGGGGGGGG   
  | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRES GENERAL TIPVGPLGKV  361 GAGATCCIGAACTACAGGGTIGAGACGGGTGTCCTGCAAGAGGAGTGTGTGCCCATGCCGGGGGCCCCGGGGCCAGGGTAAGGGGGAAGCCAGGTTGCCCTTGACGAGGGGGAGGGTGAGGGGTAAGGGGTGGGGAAGCGTGTGCCCTTGACGAGGGGAACCGGGTGAGGGTAAGGGGTGGGGAAGCCGGGGGAGGTAGGGGGAAGCCAGGTTAGACCTACAGGGGTGTAGACGTAGAGCTGGTGCCCTGCGGGGGCCCGGGGCCCAGGGTAAGGGGGAACCCAGGGTGAGGGGGAACCCCGCAATTGCACTAGGGAACACCAGGGGGGGAACCCCCAAGGGTGGAGAGGGGGGGAACCCCGCAAGGTAAGGAGAGAGA   | CIVGLS NKLTVMDNIG DSGVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRESGETTGAGAGGGTTGAGAGGTTGAGAGGGTGTGAGGTGAGGGTGAGGGGGG   | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQRKVVTTDQFVINHHQARRERGELTGETGETGEGGGGCCTGGGGGCTGAGGGGGAGGGTATGGGGGAGGGGGGGG   | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGECGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | CIVGLS NKLTVMDNIG DSGVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRESGETTGAGAGGGTTGAGAGGTTGAGAGGGTGTGAGGTGAGGGTGAGGGGGG  
  | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRES GENERAL TIPVGPLGKV  361 GAGATCCIGAACTACAGGGTIGAGACGGGTGTCCTGCAAGAGGAGTGTGTGCCCATGCCGGGGGCCCCGGGGCCAGGGTAAGGGGGAAGCCAGGTTGCCCTTGACGAGGGGGAGGGTGAGGGGTAAGGGGTGGGGAAGCGTGTGCCCTTGACGAGGGGAACCGGGTGAGGGTAAGGGGTGGGGAAGCCGGGGGAGGTAGGGGGAAGCCAGGTTAGACCTACAGGGGTGTAGACGTAGAGCTGGTGCCCTGCGGGGGCCCGGGGCCCAGGGTAAGGGGGAACCCAGGGTGAGGGGGAACCCCGCAATTGCACTAGGGAACACCAGGGGGGGAACCCCCAAGGGTGGAGAGGGGGGGAACCCCGCAAGGTAAGGAGAGAGA   | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGACATGGCGTTTAACGACGGTGTCTGGAACAGGATGTTGTGCCCATGTGGCGCGCGC  | CIVGIS NKLTVMONIGOS SOVISSER PRRISEAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGECCACTGGAACTACAGGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACTTCACCGAACTACAGGGTTGACGTCAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACTTCACCACACACA   | CIVGIS NKLTVMONIGOS SOVISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGECCACGGGGCCCAGGGGCCCAGGGGCCAGGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGCAGGCCAGGCCAGGCCAGGCAGGCCAGGCA | CIVGIS NKLTVMONIGOS SOVISSFKPRRISFAPYSAPQLE 
LDQVVPNLHRKVVTDQFVINHHQARRERGEGECCACGGGGCCCAGGGGCCCAGGGGCCAGGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGCAGGCCAGGCCAGGCCAGGCAGGCCAGGCA | CIVGIS NKLTVMONIGOS SOVISSER PRRISEAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGILS NKLTVMONIGOS S VISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRESSTERSECCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGILS NKLTVMONIGOS S VISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRESSTERSECCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGLSNKLTVNDNIGSDSGSVACGCTTAACGACGCTTAACGACGCTTAACGACGCTATTACCTAAGGGGCTAACGCCCTGGGGCCCAGGGCCCAGGGCCCAGGGGCCAGGGCCAGGCCCAGGACCCCATTTTTCCCTTCTCTCTTTTTCCCTTATTTCCCAGGGGCCAACTTTTTCCCTTGAGGGCTTAACGACGCTTTTTCCCTTGAGGGCTAACGCCAGGTTTTTCCCTTGAGGGCTAACGCCAGGTTTAACGACGGTTAACGACGCTATTTCCCTTGAGGGCTAACGCCAGGTTAACGACGCTATTTCCCTTGAGGGCTAACGCCAGGGCCAGGGCTAACGCCGCGCCCAGGGCCAGGCCAGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCACCTGAACGCCAGGCCAGGAGCCACTGAGGAGGCCACTGAGGAGGCCACTGAGGAGGCCACTGAGGGCCACGCAGGAGCAGGCCAGGAGCACCTTCCAGGGGGCAACCCAGGAGGCCACTGAGGAGCACCAGGAGGCCACCGCAGGAGAGCCACCAGGAGG  | CIVGLSNKLTVNONIGOS SGVISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTTDQFVINHHQARRESCGCCCCCCCCGGGCCCCGCGCCCCCCCCCCCGCGCCCCCC   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICETGACATACAGGGTTGAGATGGGGTGTCCTGGAGAGAGATTGTGGCCGGGCCTGGGGGCCAGGCTGAGAGTATGGGGAGATGGCCTTRAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCTCAGCTTGCGCGGGGATATTGCGATAAGGCAGTTTAGGGGTTGTGTGAGTGA   
   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICETGACATACAGGGTTGAGATGGGGTGTCCTGGAGAGAGATTGTGGCCGGGCCTGGGGGCCAGGCTGAGAGTATGGGGAGATGGCCTTRAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCTCAGCTTGCGCGGGGATATTGCGATAAGGCAGTTTAGGGGTTGTGTGAGTGA   | CIVGIS NKLTVMONIGOS SOVISSER PRRISEAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGIS NKLTVMONIGOS SOVISSER PRRISEAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGILS NKLTVMONIGOS S VISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRESSTERSECCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGLS NKLTVNNONIGOUS GVISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHRKQVKTDQFVINHHQARREGGGCCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGCCCAGCCCCCC   | C I V G L S N K L T V M O N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGCCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTCCCAGGCCGCGCCTCGCGGCCCAGCGTAATGGGGACGCCATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCCTTCGCGACATATGCGATAAGGCACTTAAGGCTGTTCTGAGTGTCTGATGTGAGTGTGCACTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGTTGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAAGGAGTTGGGGGCCAACCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H GRE'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P P S S S  Element D .  841 ATTGACCCTGAGCTGTGCAGCCGCACCTCTGAGGCTTAACTCTGAGGCTAACCTAGGGCCAATTTTTTCCCTGGATTTTTGCCTGGATTTTTGCCTGGATTTTTTCCTGGATTTTTTGCCTGGATTTTTTTT | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGCCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCAGGCCGCGCCTCGCGGCCCAGCGTAATGGGGACGCCATGACCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L 
CTCCTCAGCCTCGCGCGCAATATGCGATAAGGCAGCTTTAAGGGCTTTTAAGGTCTGATGTGTGTG  | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGCGCTCGGGGCCCAGGGTAATGGGGGACECCAGGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGGCTTGCGGGCGGATATTGCGGATAGGGAGGTTGTGTGCAGTGTGAGTGTGTGAGGGATGAGGATGTTGTAGGTTAATTAACGAGGTAATTGAGGATG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L K P A V G E  601 TTGAGGGACACACCAGAGACTCTCTGTAGGCGTACTGTGACCTCCCAGGGGGGTTGAGATATATAGGAAGTTACAACAGATGCCGAGAGGAGGAGCTTTGTGGGGGAACTCTTGTAGGCCTCTTGTAGGCTTAGAGACTTAGGGGGGGTTGAACAGAATGCCAGAGAGAG  | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGCAGGGGTGCCTGGAGAGGAGGATGTTGTGCCCACTGGGGGCCTGGGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGCGGATATTGCGGATAGGGAGGTTAGAGGTTAGAGGTGTTGTCAGGAGTGAGGATGGGGAGGTAGGGATGTGGTTATATAGGGGTAGGTTAGTGAGATG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  601 TTGAGGGACAACCCAGAGATCCTCCTGAGGGGTACTCCCCAGGGGGTTACCCCCACTGAGATATATAGGAGTACAACAAGATGCCCGAGGAGAGACTTTGCCCTCTAGGGGGTACTCCCAGGGGGGTTGCAGCAGGAGTTCAACAAGATGCCCGAGGAGAGACTCCTCTTCCTCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H GRF6'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTTGAACTCTATGGCCTTCTCAGGGGGCACTTCCGCGTGGGGAGGGGGGGG   | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTTGAAGAGGAGGTGTTCCTGGAAGAGGATGTTGTGCCACTGTGCCCGCGGCCCAGGGTAATGGGGAGACCAGGTTTGACCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGGGATATTGCGATAAGGCAGGTTTCTGTGTCAGTCA  | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGTAGGCGTTTAACGACGGTGTCCTGGAAGAGCATGTTGTGCCCTGGCGGCCCAGGGTAATGGGGAGGCCAGGGTAATGGGGAGACCCCAGGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGCGCGGATATTCCGATAAGGCAGCTTAAGGTGTTTCCAGTGAGTG  | C I V G L S N K L T V M D N I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGCCCTCGCGGCCCAGGGTATGGGGAACGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGATGTGTGAGGGATGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTAAGTATATTGAGCAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L R G L L K P A V G E  1720 TTGAGGGACAACCAGAAGTCCTCCTGTACGCCGTCAGGCGGGGGGGG  
   | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGTGCGCGGCCCAGGGCAATGGGGAACGCCAGGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCGATATTGCGATAAGGCACCTTAAGGGTGTTGTCAGTGAGTTGAGTGAG   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTCCCACTGTGCGCGGCCCCAGGGCAATGGGGAACGACGACGCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGTGTTTCAGTGAGTCTGATGTGGCGACTGATGAGGTTGAGTTGAGTTTAACGAGGTGTTATATCAGGGTGTTTATACAGGGTGTTTAACGACACCAGATTGAGCAGCTTCAGGGTGTTAGGGTGGGGAACGACCTTTAAGGATTGAGACAGAGTGTTAGGGGGAACAACAAGAGTGCGAACAACAAGAGTGCGAACAACAAGAGTGCGAACAACAAGAGAGAG | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTCCCACTGTGCGCGGCCCCAGGGCAATGGGGAACGACGACGCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGTGTTTCAGTGAGTCTGATGTGGCGACTGATGAGGTTGAGTTGAGTTTAACGAGGTGTTATATCAGGGTGTTTATACAGGGTGTTTAACGACACCAGATTGAGCAGCTTCAGGGTGTTAGGGTGGGGAACGACCTTTAAGGATTGAGACAGAGTGTTAGGGGGAACAACAAGAGTGCGAACAACAAGAGTGCGAACAACAAGAGTGCGAACAACAAGAGAGAG | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCACTGTGCGCGGCCCAGGGTCAGGGGGCCCAGGGTAATGGGGGACCCAGGTTAAGGGTTTAACGACGGTTTCTGGCAAGACCATGTTGTGCCACTGTGCCGCGCGCTCGGGGCCCAGGGTAATGGGGGACCCTGAGGTTTAAGGCTTGAGTTTAAGGCAGTTGTAAGGATGTGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGGAGGTTGAGAGTTTAAGGAAGTAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGAAGTAGAGAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGAAGTAGAGAGAGAGAGAGAACCAGAAAGAGAACCAGAAAGAA  | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCACTGTGCGCGGCCCAGGGTCAGGGGGCCCAGGGTAATGGGGGACCCAGGTTAAGGGTTTAACGACGGTTTCTGGCAAGACCATGTTGTGCCACTGTGCCGCGCGCTCGGGGCCCAGGGTAATGGGGGACCCTGAGGTTTAAGGCTTGAGTTTAAGGCAGTTGTAAGGATGTGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGGAGGTTGAGAGTTTAAGGAAGTAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGAAGTAGAGAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTAAGGAAGTAGAGAGAGAGAGAGAACCAGAAAGAGAACCAGAAAGAA  | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P M L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTTCAGATGCGCTTTAACGACGGTTCTCTGGAAGACCATGTTGTGCCACTGTGCGCGCGC  | CIVGLS NKLTVMOMIGOSGVISS FKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGLTIPFYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGCCTCTGGAGACACGTTTCTGCAAGACACGTTTGTGCCAGGCCCCCGGCGCCCCGGCGCCCAGGGTAATGGGGAACGCCAGGTTAACGACGGTTTAACGACGGTTCTGCAAGACACAGTTTGTGCCAGGCGCCCCGGGCCCCAGGGTAATGGGGAACCCAGGTTAACGACGCTTTAACGACGGTGTTTGCCCGAGGACACTGTTGTGCCAGGCCCCCCGGCCCCCGGCCCCAGGGTAATGGGGACGCCAGGTTAACGACGACGCCAGGTTAACGACGCCCCCCTGAACGACGCCCCCCTGAAGGACACGCCCCCCTGAAGGACGACGCCAGGTTAACGAGGTTGAGGTTCAAGGAGTTCAACAAGAAGATGCCCCCACTGAAGACACAAGATGAACAAGAAGATGCCCCAAGATACACAAGATGACACAAGATGACACAAGATGACACAAGATGCCCCCAGGAACACCCCCCCTTTTCCCCAGCTCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCATGTTTGGGGGCCACGCCCCCCTCTTTCCCTCTCTCCCCCCTTTCCCCAGCTCCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAGTTTCCCTCCTCTCCTCCCCCTTTTCCCTCTCTCCTCTCTC  | CIVGLS NKLTVMOMIGOSGVISS FKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGLTIPFYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGCCTCTGGAGACACGTTTCTGCAAGACACGTTTGTGCCAGGCCCCCGGCGCCCCGGCGCCCAGGGTAATGGGGAACGCCAGGTTAACGACGGTTTAACGACGGTTCTGCAAGACACAGTTTGTGCCAGGCGCCCCGGGCCCCAGGGTAATGGGGAACCCAGGTTAACGACGCTTTAACGACGGTGTTTGCCCGAGGACACTGTTGTGCCAGGCCCCCCGGCCCCCGGCCCCAGGGTAATGGGGACGCCAGGTTAACGACGACGCCAGGTTAACGACGCCCCCCTGAACGACGCCCCCCTGAAGGACACGCCCCCCTGAAGGACGACGCCAGGTTAACGAGGTTGAGGTTCAAGGAGTTCAACAAGAAGATGCCCCCACTGAAGACACAAGATGAACAAGAAGATGCCCCAAGATACACAAGATGACACAAGATGACACAAGATGACACAAGATGCCCCCAGGAACACCCCCCCTTTTCCCCAGCTCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCATGTTTGGGGGCCACGCCCCCCTCTTTCCCTCTCTCCCCCCTTTCCCCAGCTCCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAGTTTCCCTCCTCTCCTCCCCCTTTTCCCTCTCTCCTCTCTC  
   | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H W Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGCCGTTTAACGACGGTGTCCTGGAAGACCATGTTGTGCCAGGGCGCCTCGGGGCCCAGGGTAATGGGGAGCCCAGGTATGCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGCGCATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGTTTAACGGCGTAGTATGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGAACACCAGAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGAGGAGCAGTTTGGGGGCAACGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGGCTTTCCCAGCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGGTTGCGGGGGGGCCGTGGGGAGGGGGGGG  | CIVGLS NKLTVMOMIGOSGVISS FKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGLTIPFYSAPQLE  LDQVVPNLHRKVVTDQFVINHWQARRERGCCTCTGGAGACACGTTTCTGCAAGACACGTTTGTGCCAGGCCCCCGGCGCCCCGGCGCCCAGGGTAATGGGGAACGCCAGGTTAACGACGGTTTAACGACGGTTCTGCAAGACACAGTTTGTGCCAGGCGCCCCGGGCCCCAGGGTAATGGGGAACCCAGGTTAACGACGCTTTAACGACGGTGTTTGCCCGAGGACACTGTTGTGCCAGGCCCCCCGGCCCCCGGCCCCAGGGTAATGGGGACGCCAGGTTAACGACGACGCCAGGTTAACGACGCCCCCCTGAACGACGCCCCCCTGAAGGACACGCCCCCCTGAAGGACGACGCCAGGTTAACGAGGTTGAGGTTCAAGGAGTTCAACAAGAAGATGCCCCCACTGAAGACACAAGATGAACAAGAAGATGCCCCAAGATACACAAGATGACACAAGATGACACAAGATGACACAAGATGCCCCCAGGAACACCCCCCCTTTTCCCCAGCTCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCATGTTTGGGGGCCACGCCCCCCTCTTTCCCTCTCTCCCCCCTTTCCCCAGCTCCCCAGGGGGACACTTCCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAGTTTCCCTCCTCTCCTCCCCCTTTTCCCTCTCTCCTCTCTC  | C I V G L S N K L T V M O M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P M L H R K V V T D Q F V I N H M Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACTACAGGGTTCAGATGCGCTTTAACGACGGTTCTCTGGAAGACCATGTTGTGCCACTGTGCGCGCGC  | CIVGLSNKLTVMONIGOSGVISSFKPRRISFAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGCGGCGCCGGCCCAGCGCACCGGGCCCAGCGCACCGGGCCCAGCGTATGGGGGACCCCAGCGTTAACGGGTTCAGAGACCAAGACCAAGGTCCTGGAAGACCAAGACCAAGGTTGTGCCCACCTGCGGGCCCAGCGTAACGGGGACCCCAGCGTATGCGCGTTAACGGCGTTAACGACGAGACCAAGACTACAAGACTACGAGACTAACGGCGTTAAAGGAGTGTGTCCTGGAAGACCAAGATGTGAGGTTGAGGTTAACGACGGTAACGACGACTAAAGGAGTTGTACCAGGGGGTTAACGGAGTTGAGCTCCCAGGGGGGGAACCCCCCACCGGGGGGGAACCCCCCACCGGGGGG   | C I V G L S N K L T V M D M I G D S G V I S S F K P R R I S F A P Y S A P Q L E  L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATICTICAGCTICAGGGTTGAGATGGGGTGTCCTGGAAGACGATGTTGTGCCCGGGCCTGGGGGCCAGCGTATGGGGAGCCCTGTAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGCGGGATATTGCCATAAGGCAGCTTAAGGCTGTTGTGAGGATGTGTGTG   | CIVGIS NKLTVMONIGOS SOVISSER PRRISEAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGECGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  
   | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGECGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | CIVGLS NKLTVMONIGOS GVISSFKPRRISFAPYSAPYSAPQLE  LDQVVPNLHRKVVTDQFVINHHQARRERGECGECCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATICTEAACTACAGGSTTCACATCCGCTTAACGACGTTCCTGCACACACAGTTTGTGCCCGGGCCTCCGGGGCCTCCGGGGACCCCAGCGTATGGGGACCCCTAACGAGGTACGACCTACAGGGTATGCGCCCTCTGCCTCCTGCACACACA   |
| L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K  361 GAGATCCTGAACTACAGGGTTGAGATGCCTTTACGACGGTGTCCTGGAGAGAGA  | V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V TAACACACGGTGCTCCTGAAGACGATGTTGTGCCACTTGACC ARCCGTGCTCCTGAAGACGATGTTGTGCCACTTGTGCCACTTGACCCTGCGGGCCCAGCGTAATGGGGACGCCAGTATGCCCTTGACC M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D L K L T N D T L R I H P H R S I L N L N L K D P T T N L L GCAGCTTAAGGGTTGTGATGTAAGGAGTGGGGACTGAAGAGTTGAGTTTAAGGAGTTGAGTTATTAAGGATGAT   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  AGACTCTGACTCGAGGTGAGATGCGTTTAACGACGGTGTCCTGAAGACGATGTGTGCCCTGAGGACGCTGCGGGCCCAGCGTAATGGGGACGCCAGCGTTATGCCCTTGCC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGTGGGGTTGAGGCTTAGCAGCCCCTC  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTCTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCATGAGATATATAGGAAGTACAACAAGATGGCCCGAGGAGAAGTTTCTCCTGAGGGACAACTTTAGGAAGATGACAAGAAGTTGAGGGTTAACTGAGGACCCCCTT  T Q R R L S Q L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCCAGGCCCCCCATTTTTCCCTTGAGGGCTAACCTAGGGGCAACTTTCTCTGGGGTTTTTTTGCCTGTAGTTTTTTTT  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCTGAACTCAAGGGTTGAAGTGCGTTTAACGACGGTTCTGGAAGACGATGTTGTGCCACTGTGCGGGGCGCTCGCGGCCCAGCGTAATGGGGAACTGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTG  | L D Q V V P M L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V GAGAGCCTCGCGCGCCCACCTCACCTCACCTCACCTCAC  | L D Q V V P
N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGGTTTAACCACGGTGTCCTGGAAGAAGATGTGTGCCCCGGGCTCGGGGCCCAGGGTAATGGGGAAGTATGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGGATATTCCGATAAGGCACCTTATAGGGTGTTGTCAGTGAGTTCTGATGTGAGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTTGAGGGTGAGGGGGG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTCAACTACAGGATTGAGATGCCGTTTAACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTAAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTGTCAGGATTCTGATGTGAGGTTGAGGTTAAGGTAAGTTAAGGATTACAGGTTAAGTTAACAGGTTAAGTTAAGGAGTTAAGGAACTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGAA   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTCAACTACAGGATTGAGATGCCGTTTAACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTAAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTGTCAGGATTCTGATGTGAGGTTGAGGTTAAGGTAAGTTAAGGATTACAGGTTAAGTTAACAGGTTAAGTTAAGGAGTTAAGGAACTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGAA   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATCCTCAACTACAGGATTGAGATGCCGTTTAACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTAAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTGTCAGGATTCTGATGTGAGGTTGAGGTTAAGGTAAGTTAAGGATTACAGGTTAAGTTAACAGGTTAAGTTAAGGAGTTAAGGAACTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGTTAAGGAAGAA   
   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICOTGAACTACAGGGTTGAGATGCGGTTTCAGGACGAGGTTTCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCAGGGTAATGGGGAGAGTATGCCCTTGAC E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGATATTCCGATAAGGCAGCTTTAACGGGTTTCTGTGAGTTCTGATGTGAGGTTAAGGTTAAGGTTAAGTTAAGGATGTTTAAGGAGTTAAGTTAAGGTTAAGTTAAGGATGTAAGTTAAGGAGTTAAGTTAAGGAGTTAAGGATTAAGGATTAAGGAAGTTAAGGATGTAAGTTAAGGATGAAGAA  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG   
  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICOTGAACTACAGGGTTGAGATGCGGTTTCAGGACGAGGTTTCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCAGGGTAATGGGGAGAGTATGCCCTTGAC E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGATATTCCGATAAGGCAGCTTTAACGGGTTTCTGTGAGTTCTGATGTGAGGTTAAGGTTAAGGTTAAGTTAAGGATGTTTAAGGAGTTAAGTTAAGGTTAAGTTAAGGATGTAAGTTAAGGAGTTAAGTTAAGGAGTTAAGGATTAAGGATTAAGGAAGTTAAGGATGTAAGTTAAGGATGAAGAA  
   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGCACTTGTCAGGTGTTCTGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTCTGTGAGTTCTGATGTGAGGTTAAGGTACTTTAGGGGTGATATTAGGGGTGATATTAGGGGTGATATTAGAGGAG   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTCTGTGAGTTCTGATGTGAGGTTAAGGTACTTTAGGGGTGATATTAGGGGTGATATTAGGGGTGATATTAGAGGAG   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICCTGAACTACAGGGTTGAGATGCCGTTTACCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCCAGGGTAATGGGGAAGTACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCCGGGGCATATTCCGATAAGGCACCTTATAGGGGTGTTCTGTGAGTTCTGATGTGAGGTTAAGGTACTTTAGGGGTGATATTAGGGGTGATATTAGGGGTGATATTAGAGGAG   | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC   
  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC
TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC  | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCCTGAACTACAGGGTTGAACTACAGGTTTAACCACGGTTTAACCACGGTTCCTGGAACAGATGTTGTCCCACTCTGCGCGCCCCCGCGCCCCACGCGTAATGGGGACCCCTTAACCACGGTTAACCACGGTTAACCACGGTTAATGGGGACCCCCCCACTAATGGCGCCCTCAACCTCAACCACCACCACCACCACCACCACCACCA  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GACATCCTGNACTACAGGGTTTAACACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGGGGCCCCGGGGCTCAGGGTAATGGGGACGTATGCCCTTACCACGTGTAATGGGGGTTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGACGATATGGGAGGTTGAGTAGGGAGACACCAGAAGAATCCTCCTGTGAGAACCCCCCCC  | L D Q V V P N L N R K V V T D Q F V I N N N Q A R R E R G L T I P V G P I G K V  GAGATCC TGAACTACAGGGTTGACATGCCCTTTAACCACGGTTCCTGGAACAGATGTTGTGCCACTGTGCCGGCCCCGCGGCCCACGGGTAATGGGGACTGACGGTAATGGGGACTGACGACTAACGGGGTTAATGGGGACTGAACGAGTGTTAACGACGCTTAAACGACGCTTCCTGGAACAGAACAGTGTTGTGCCCTGACGCGCCACGCGGAACTGAACGGGGTTAATGGGGGACACCAGAACAGAACAGAACAGAACAGAACACCAGAACAGAACACCAGAACAGAACACCAGAACACCAGAACAGAACACCAGAACCACC   
   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCC TGAACTACAGGGTTTAACTACGGCTTTAACCACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGCGGCCCCAGGGTAATGGGGACCAGTATGCCCTTACCACGGTGTAATGGGGGACGTCAATGGGGGACCAGTATGGCGCTCACGACGTAATGGGGGACCAGTATGCCCTTACCACGTCAATGGACGTTAATGGGGGACAGACGATGTCAGTTGAGAGAGAGTTGAGAGAGAGTTGA   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GACATCCTGNACTACAGGGTTTAACACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGGGGCCCCGGGGCTCAGGGTAATGGGGACGTATGCCCTTACCACGTGTAATGGGGGTTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGTAATGGGGGACGACGATATGGGAGGTTGAGTAGGGAGACACCAGAAGAATCCTCCTGTGAGAACCCCCCCC  | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCCTGAACTACAGGGTTGAACTACAGGTTTAACCACGGTTTAACCACGGTTCCTGGAACAGATGTTGTCCCACTCTGCGCGCCCCCGCGCCCCACGCGTAATGGGGACCCCTTAACCACGGTTAACCACGGTTAACCACGGTTAATGGGGACCCCCCCACTAATGGCGCCCTCAACCTCAACCACCACCACCACCACCACCACCACCA  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  GAGATICOTGAACTACAGGGTTGAGATGCGGTTTCAGGACGAGGTTTCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCAGGGTAATGGGGAGAGTATGCCCTTGAC E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGGGGATATTCCGATAAGGCAGCTTTAACGGGTTTCTGTGAGTTCTGATGTGAGGTTAAGGTTAAGGTTAAGTTAAGGATGTTTAAGGAGTTAAGTTAAGGTTAAGTTAAGGATGTAAGTTAAGGAGTTAAGTTAAGGAGTTAAGGATTAAGGATTAAGGAAGTTAAGGATGTAAGTTAAGGATGAAGAA   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG   
  | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GACATCCTCAACCTACAGGGTTGACGTACACCAGGTGTTCTGCAACACCAGTGTTGCCCCGGGCCCGGGCCCGGGCCCAGGGTATGGGGACGTATGCCCTTGACCTACAGGGTGTTCTGAACACAGGTGTTCTGCAACACACGTGTTGCCCGGGCCCAGGGTATGGGGACGTATGCGGATTACCCCTTGACCACCGGGTTTCCCGGGGCCCAGGCTCAGGGTATATGGGGATGCCCTTGACGACGACCTTTACCGAACACCGTTACAGCAACCACCTTCAACGTACAGCAACCTTCCAGGGTGTTCTCCCAGGGTGAGGTTACCCTCTAGGGATTCTCCCAGGGTGAGTTTCCAGGATACTTTCCCCAGGGTTACATTCGCGGGATTTTCCGCTTCCCCCCCC  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GACATCCTCAACCTACAGGGTTGACGTACACCAGGTGTTCTGCAACACCAGTGTTGCCCCGGGCCCGGGCCCGGGCCCAGGGTATGGGGACGTATGCCCTTGACCTACAGGGTGTTCTGAACACAGGTGTTCTGCAACACACGTGTTGCCCGGGCCCAGGGTATGGGGACGTATGCGGATTACCCCTTGACCACCGGGTTTCCCGGGGCCCAGGCTCAGGGTATATGGGGATGCCCTTGACGACGACCTTTACCGAACACCGTTACAGCAACCACCTTCAACGTACAGCAACCTTCCAGGGTGTTCTCCCAGGGTGAGGTTACCCTCTAGGGATTCTCCCAGGGTGAGTTTCCAGGATACTTTCCCCAGGGTTACATTCGCGGGATTTTCCGCTTCCCCCCCC  | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GACATCCTCAACTACAGGGTTGACGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCCCGGGCCCGCGGCCCGGGGCCCGGGGCCCGGGGCCCGGGTATTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCACCTTAAGGGTTTGTCAGTGGAGTTCAATGAGGATGGCCCACTGATGAGGTTAAGGTTAATTGAGGAG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  10 TGGGGGACAACCAGAAGATCCTCCTGTACGCCTCATGACCTCCCAGGGGGGGTTAACTGAGATTAATAGGAAGTACAACAAGATGGCCGAGGAGAGCAACCAGAAACCCTCCTGTAGGGGGAACCCCCCCC   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V 
ARCHITECTERACTACAGGETTGAGATCCCTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCAGGGTAATGGGGGACGCTTTAACGACGTTTACCACAGGTTTACCCACGGTGTCCTGGAAGACGATGTTGTGCCCGGGCTCGCGGCCCAGGGTAATGGGGGACGCTTTAACGACGTTACCCTTTACCACGACGACGTATTGCCGTAAGGACGTTAACGACGTTACGAGGATTTAACGCATTTACAGGATTTACAGGATTTACAGGATTTACAGGATTTACAGGATTACAGGATTACAGGATTACAGGACTTCCCAGGGGGGAACCCCCACTGAAGATTACAGGATTACAGGATTACAGGAACAGATGCCCCCCACTGAAGATACCAAGGATACCACAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGGATACCAAGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V GACATCCTGAACTACGGGTTGACGACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACACGATCTTGAACACACAC   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V GACATCCTGAACTACGGGTTGACGACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGTTAACGACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACGATCTTGAACACACGATCTTGAACACACAC   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GACATCCTCAACCTACAGGGTTGACGTACACCAGGTGTTCTGCAACACCAGTGTTGCCCCGGGCCCGGGCCCGGGCCCAGGGTATGGGGACGTATGCCCTTGACCTACAGGGTGTTCTGAACACAGGTGTTCTGCAACACACGTGTTGCCCGGGCCCAGGGTATGGGGACGTATGCGGATTACCCCTTGACCACCGGGTTTCCCGGGGCCCAGGCTCAGGGTATATGGGGATGCCCTTGACGACGACCTTTACCGAACACCGTTACAGCAACCACCTTCAACGTACAGCAACCTTCCAGGGTGTTCTCCCAGGGTGAGGTTACCCTCTAGGGATTCTCCCAGGGTGAGTTTCCAGGATACTTTCCCCAGGGTTACATTCGCGGGATTTTCCGCTTCCCCCCCC  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P Y G P I G K V  361 GAGATCCTGAACTACAGGGTTGAACTACAGGGTTTAACCACGGTGTCCTGGAACAGCGTGTTGTGCCCCGGGGCCTCGCGGCCTCGCGGGCCTAATGGGGGACCCTTCACCAGTTATGCCCTTCAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGGCGCATATTGCCATAAGCCACTTAAGGGTGTTCAGTGATCTGATGTGAGGATGCAGCTGAACAGGTTGAGGTAGAGAACAGAGAGTTGCCCTGAGGAGCAGCCCTCAGGAGCAGCCCTCCCCCCCC   
   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E A G L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E A G L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R M G D A R Y A L D E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R M G D A R Y A L D E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R M G D A R Y A L D E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R M G D A R Y A L D E I L N L N L K D P T T N L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q C TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E A G L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E A G L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V E A G L D Q V V P L C A A L A A Q R H G D A R Y A L D L R I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R H G D A R Y A L D L CICCICAGCITCAGGGGGGGGGGGGGGGGGGGGGGGGGGG   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCTGAACTACAGGGTGAAGACGCGTTTAACGACGAGGTCTCTGAAGACGATGTTGTGCCACTGTGCCCGCGCCCAGCGTAATGGGGAGCCAGCGTTAATGGCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGGTGTTGATGAGGTGTGAGGTGGGGAGTGAGGGGTTGAGGGTTGAGGTTGAGGTTGAGGTTGAGCAGTATTAAGGAGTTTAAGGATTTAAGGAGTTTAAGGATCTCTCTGCGGCGAAGATCCTCCTAGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGAGAGAGAGAGAGAGAAGA  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V E A G L T I P V G P I G K V E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D E A A L S F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D E A A L S F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D E A A L S F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D E A A L S F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D GO D A R Y A L D E I L N L N L K D P T T N L L CTCCTCAGCTTCGCGGCGGATATTGCGATAGGCAGCTTAAGGCTGTGTGAGGTTGAGGAG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGAGGCGTTTAACGACGGTCTGGAGAACGATGTTGTGCCCTGAGCGCGCCTGGGGGCCAGCGTAATGGGGGACGCCTGAACGAGGTTAACGAGGTTAACGAGGTTTAACGACGGTCTGGAAGAACATTTTGTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTGTGTG   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAAGGGGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCACTGTGCGGGCCCAGGGTAATGGGGGAACCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCACTTAAGGCTGTTGTCGAGTCTGAGTGTGAGTTGAGTTGAGGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTCTGAGTGAG  
  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCACTGTGCCGGGCCCTCGCGGCCCAGGGCTCAGGGAACGACGTTAATGGCCATTGACCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGCGGGGATATTGCCATAAGCAGCTTAACGCTTGTGATGATGATGTGTGTG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGTGGGGTTAACGACGTGTCCTGGAGAGCGATGTTGCCCACTGGGGCCCCGGCCCCGGCCCAGGGTATGGGGACCCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGCGGATATGCGATAAGGCAGCTTTACAGGTGTTGTCACTCAGTGTGTGT   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGCGCTTTAACGACGGTTGCCTGAGAGACGATGTTGTGCCCACTGTGCGCGCCCCAGCGTAATGGGGAGCCCAGGTATGCCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGCGCGGATATTGCGATAGGCGACTTTAAGGCTGTTGCAGTGAGTTGTGCTGATGTGGGCACTGAGTGAG   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGCGCTTTAACGACGGTTGCCTGAGAGACGATGTTGTGCCCACTGTGCGCGCCCCAGCGTAATGGGGAGCCCAGGTATGCCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTGCGGCGCGGATATTGCGATAGGCGACTTTAAGGCTGTTGCAGTGAGTTGTGCTGATGTGGGCACTGAGTGAG   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTGTCCTGGAAGACGATGTTGTCCACTGTGCGCGGCGCTCGGGGCCCAGGGTAATGGGGAACCCCTGAGATGGCGCTTAACGAGGTTCAGGAGACGATGTTGTCCCTGAAGACGATGTTGTCCCACTGTGCGCGGCCCCAGGGTAATGGGGAACCCCCTGAACGAGGATGAGGCAACCAGGATATGGCGATATGGCGCATTAAGGCAGCTTAAGGATGTGAGGTTGAGGCAGAGACCCCCCTC  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGCACAACCAGAAGACCCCCTGTACGCCCTCCTGAGCCTCCCCAGGGGGGGTCCCCCCACTGAGATATATAGGAAGTACCACAAGAGTGCGCGAGGGGAGAGGGGGGAAACCCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H ORF8'  721 ACGCAGAGGAGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTTATGGCCTTGTGGGAATTGAGGATTGTTGCCGGGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTGTCCTGGAAGACGATGTTGTCCACTGTGCGCGGCGCTCGGGGCCCAGGGTAATGGGGAACCCCTGAGATGGCGCTTAACGAGGTTCAGGAGACGATGTTGTCCCTGAAGACGATGTTGTCCCACTGTGCGCGGCCCCAGGGTAATGGGGAACCCCCTGAACGAGGATGAGGCAACCAGGATATGGCGATATGGCGCATTAAGGCAGCTTAAGGATGTGAGGTTGAGGCAGAGACCCCCCTC  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGCACAACCAGAAGACCCCCTGTACGCCCTCCTGAGCCTCCCCAGGGGGGGTCCCCCCACTGAGATATATAGGAAGTACCACAAGAGTGCGCGAGGGGAGAGGGGGGAAACCCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H ORF8'  721 ACGCAGAGGAGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTTATGGCCTTGTGGGAATTGAGGATTGTTGCCGGGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTAACGACGGTGTCTGGAAGACGATGTTGTCCCCACTGTGCGCGCCCCAGGGCCCAGGGTAAGGGGAACCCCTGAGGTTAACGACGGTTTAACGACGGTTCTGAGAGACGATGTTGTCCCCACTGTGCGCGCCCCAGGCTCAAGGGGAACCCCAGGTATGGCGATGCCCCTGAAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCCTTCGCGGCGCGATATTGCGATAAGGCAGCTTAAGGGGTTTGTCCTGAGTCTGAGTCTGAGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGTTTAACGCAGG L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGACAACCAGAAGATCTCCTGTACCCCGTCCTGAGCCTCCCAGGGGGGGG  | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTTGTCTGGAAGACGATGTTGTGCCCACTGTGCGGGCCCAGGGCCCAGGGTAATGGGGAACCCCTGAGCTTGAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGCGGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGTGAGTCTGAGTGTGAGGAGGGGGGGG   
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   | L D Q V V P N L H R K V V T D Q F V I N H H Q A R R E R G L T I P V G P I G K V  361 GAGATCCTCAACCTACAGGGTTGAGATCGCGTTTACGACGGGTTCTCTGAAGACGATGTTGTGCCCGGGCCCGGGGCCCGGGGCCCGGGGCCCGGGCCCAGGTATGGGGGATGACCTTTACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  481 CTCCTCAGCTTCGCGGGGGATATTCCGATAGGCACCTTAAGGACGTTGTGTCAGGATCTCTATGTGAGGTTGAGGTTGAGGTTGAGGTAGATTTCAGGGGTTTTTCCGCGGGGATATTCCAGGATCTTCAGGATCTTCAGGATCTCAGGTTGAGGGGGG | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCC TGAACTACAGGGTTTAACTACGGCTTTAACCACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGCGGCCCCAGGGTAATGGGGACCAGTATGCCCTTACCACGGTGTAATGGGGGACGTCAATGGGGGACCAGTATGGCGCTCACGACGTAATGGGGGACCAGTATGCCCTTACCACGTCAATGGACGTTAATGGGGGACAGACGATGTCAGTTGAGAGAGAGTTGAGAGAGAGTTGA | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCC TGAACTACAGGGTTTAACTACGGCTTTAACCACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGCGGCCCCAGGGTAATGGGGACCAGTATGCCCTTACCACGGTGTAATGGGGGACGTCAATGGGGGACCAGTATGGCGCTCACGACGTAATGGGGGACCAGTATGCCCTTACCACGTCAATGGACGTTAATGGGGGACAGACGATGTCAGTTGAGAGAGAGTTGAGAGAGAGTTGA | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R 6 L T I P V 6 P I 6 K V  361 GAGATCC TGAACTACAGGGTTTAACTACGGCTTTAACCACGGTGTCCTGGAACACGATGTTGTGCCACTGTGCGCGGCCCCAGGGTAATGGGGACCAGTATGCCCTTACCACGGTGTAATGGGGGACGTCAATGGGGGACCAGTATGGCGCTCACGACGTAATGGGGGACCAGTATGCCCTTACCACGTCAATGGACGTTAATGGGGGACAGACGATGTCAGTTGAGAGAGAGTTGAGAGAGAGTTGA   | L D Q V V P N L H R K V V T D Q F V I N H N Q A R R E R G L T I P V G P I G K V  361 GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACAGGGTGTCTGGAGACAGATGTTGTGCCTGGGGGCTCGCGGGCCTCGGGGCCCTGGGGGCCTCGGGGCCTCGGGGCCCTGGGGGCCTCGGGGCCCTGGGGGCCGCC   |
| GAGATCCTGAACTACAGGGTTGAGATGACGGTGTCCTGAAGACGATGTTGTGCCCACTGGGGGCCCTGGGGGCCAGGGTAATGGGGGACGCCATGCCTTG E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCAGTGAGTTGATGTGAGGTGGGGACGAGGAGGTTGAGGAG   | TAACGACGGTGTCCTGGAAGACGATGTTGTGCCCACTGTGCGCGCCCCAGCGTAATGGGGGACGCCAGGTATTGCCCTTGAC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GCAGCTTAAGGGTGTGTCAGTGGAGTGTGATGTGAGGTGGCGACTGAGAGGTTGAGGTTGAGGTTTATCAGGCAGTATTGAGCAG  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  CSTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAAGAAGGAGGGGGGGG  | ### STATES OF THE PRODUCT OF PROD | 81 GAGATCCTGAACTACAGGGTTGAGATGCGTTTAACGACGGTGTCCTGGAGAGACGATGTTGTGCCCGGGGCTCGGGGCCCAGGGTATGGGGAACGCCAGGTTTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATTTGCGATAAGGCAGCTTAAGGGTGTGTCAGTGTGTGT  | ### A FIND G V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E D N Q K I L L Y A V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L A AGGREGATION TOCKNESSES TO CONTROL T | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAGGCCAGGGTTAACGACGTTTAACGACGGTGTCCTGGAAGACGCAGGTTGTGGGGACGCCCAGGGTATGGGGGACGCCCAGGGTATGAGGACGCAGGTATGAGCAGGACGCCCTCAGGGTTTAACGAGGTTGAGGGTTTACGAGGTTGAGGTTGAGGTTAACGAGGTAGGAAGCAGCCCTCCAGGGTTAACGTTGAGGGTGAGGATGTTGAGGGTGAGGATGAGGAAGCAGCCCCTCCAGGGGACAACCAGAAGAAGAAGAAGAAGAAGAAGAAGA  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  
   | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCAGGGGACACCCCAGGACACCCCACGACACACACACACAGGGGCCCCCC  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCAGGGGACACCCCAGGACACCCCACGACACACACACACAGGGGCCCCCC  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCAGGGGACACCCCAGGACACCCCACGACACACACACACAGGGGCCCCCC  | ### ACCCCAGACCTGAACTTCAGGGTTGAAGGGGTTTAACGGGGGTCCTGGAAGACGATGTTGTGCCCACTGTGCGGGGCCCAGGGTAATGGGGGACGCCAGGTTTGCCCTTGAGGACGCCAGGTTAACGAGGTGTTGTGCCCTTGAGGACGCCAGGTTAACGGAGTTGAGGACGCAGGTTAAGGGTGTTAACGGGTGTTGTGCAGGTTGAGGACGCAGGTTAAGGGTGTTAACGGGTGTTAACGGTTGTGCAGGTTGAGGACGCAGGTTAAGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG  
  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCAGGGGACACCCCAGGACACCCCACGACACACACACACAGGGGCCCCCC  | ### ACCCCAGACCTGAACTTCAGGGTTGAAGGGGTTTAACGGGGGTCCTGGAAGACGATGTTGTGCCCACTGTGCGGGGCCCAGGGTCATGGGGGACGCCAGGTTTGCCCTTGAGGACGCCGCCAGGGTATGGGGGACGCCAGGTTAACGAGGTGTTGTGCCCTTGAGGACGCAGGTTAACGGTGTTTTCCTTTTACCTTAAGGACGTGTTTTTGCAGGACGCCCTATCTGCAGGTTTTTGCAGGACGCCCTATCTGCAGGTTTTTGCAGGACGCCCTTATACTTTTACAGGACGTTTTTTTT   | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  
   | ### ACCCAGAGGACTTCAGGCTTTAGGCGTTTAGGCGGTGCTCTGGAGGACGACGTTTGGCCCACGTGTCCGCGGCCCAGGGTATGGGGACGCCAGGTTTGCCCTTGAGGCGGTCCAGGTTTGGCCTTGAGGCGTGCCCAGGTTATGGGGGACGCCAGGTTTAGGCGGACGCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCCAGGTTTAGGGGGACGCCAGGTTTAGGGGGACGCCCAGGTTAGGGTTTAGGGGGACGAGGAGGACGCCCAGGGGACACCCAGGGGACACCCAGGAGAGACACCCAGGAGACACCCAGGACACCCCAGGGGACACCCAGGAGACACCCAGGAGAGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGGGACACCCCAGGACACCCCAGGACACCCCCACGGACACCCCCACGACACACACACAGGGGCCCCCC  | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### STANDARD CONTROL OF THE PROPERTY OF THE PR | GAGATCCTGAACTTGAGGGTTGAGATGACGGTTTACCACGGTGTCCTGGAAGACAGTGTTGTGCCACTGGCCGGGCCCAGCGTATGGGGACGCCTTGACCTTGACCTTGACCCTTGACCTTGACGCCGAGCCAGCTTATGGGGGCAACGCCCTTGAGAGTATGCCCTTGACCCTTGAGGGTGTCTCTATGTGAGGAGGTGCCCCAGCGTATGGGGCAACGCCCTAAGGGTGTCTCTATGTGAGGTGAGGTCTGAGGGTGCAGGGTGCCCAGCGTATGGCCATAGGGCACTTAAGGGGGGGG  | ### BASE OF THE PROPERTY OF TH  | GAGATC TEACHTACAGGSTTGAGATGACGATTACACACGGTTTACCACAGACACGTTGTCCTGAAGACAGATTGTGTCCATTGTCCCGGGCCCAGCGTAATGGGGACGCCTTGAACCACGAGATCACGAGATCACTTGAGGGCCAGCCTCAGGGCCAGCCTAAAAAAAA   | GAGATCCTGAACTTGAGGGTTGAGATGACGGTTTACCACGGTGTCCTGGAAGACAGTGTTGTGCCACTGGCCGGGCCCAGCGTATGGGGACGCCTTGACCTTGACCTTGACCCTTGACCTTGACGCCGAGCCAGCTTATGGGGGCAACGCCCTTGAGAGTATGCCCTTGACCCTTGAGGGTGTCTCTATGTGAGGAGGTGCCCCAGCGTATGGGGCAACGCCCTAAGGGTGTCTCTATGTGAGGTGAGGTCTGAGGGTGCAGGGTGCCCAGCGTATGGCCATAGGGCACTTAAGGGGGGGG  | ### BACECTEGACTTACAGGGTTGAGATGACGTTTACCACGGTTCTCTGAGAGACAGATGTTGTGCCATGTGCCGGGCCCAGCGGCCAGCGTAATGGGGACAGCCTTGACCAGAGACTAGAGATGAGAGATGAGAGATGAGAGAGA   
  | ### ACCCCAGACCTGAACTTCAGGGTTGAAGGGGTTTAACGGGGGTCCTGGAAGACGATGTTGTGCCCACTGTGCGGGGCCCAGGGTCATGGGGGACGCCAGGTTTGCCCTTGAGGACGCCGCCAGGGTATGGGGGACGCCAGGTTAACGAGGTGTTGTGCCCTTGAGGACGCAGGTTAACGGTGTTTTCCTTTTACCTTAAGGACGTGTTTTTGCAGGACGCCCTATCTGCAGGTTTTTGCAGGACGCCCTATCTGCAGGTTTTTGCAGGACGCCCTTATACTTTTACAGGACGTTTTTTTT  | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGGCTATGTGCCCACTGTGCCCGGGCCCAGGGTCATGGGGGACGCCAGGGTATGCCCTTGAC ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q ### Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E ### CTCCTGAGGCACACCAGAGACTCTCCTGTAGGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAGTTCAACAGATGCCCCAGGGGCCAGTTCAGACTACAGACTGCCCCAGGGGCCACTGGAGAGACTCCCCCTGTGAGGGCCATCCCCAGGGGGGTACCCCCACTGAGATATATAGGAGAGTACAACAGATGCCCCAGGGGCCAGTTCAGACTACAGATTCCAGGGGGCCCCCCTC ### A CGCAGAGGGAGGCCTTTCCCAGGCGAACTCGAGGGGGGGG  | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGGCTATGTGCCCACTGTGCCCGGGCCCAGGGTCATGGGGGACGCCAGGGTATGCCCTTGAC ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q ### Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E ### CTCCTGAGGCACACCAGAGACTCTCCTGTAGGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAGTTCAACAGATGCCCCAGGGGCCAGTTCAGACTACAGACTGCCCCAGGGGCCACTGGAGAGACTCCCCCTGTGAGGGCCATCCCCAGGGGGGTACCCCCACTGAGATATATAGGAGAGTACAACAGATGCCCCAGGGGCCAGTTCAGACTACAGATTCCAGGGGGCCCCCCTC ### A CGCAGAGGGAGGCCTTTCCCAGGCGAACTCGAGGGGGGGG   | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGGCTATGTGCCCACTGTGCCCGGGCCCAGGGTCATGGGGGACGCCAGGGTATGCCCTTGAC ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q ### Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E ### CTCCTGAGGCACACCAGAGACTCTCCTGTAGGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAGTTCAACAGATGCCCCAGGGGCCAGTTCAGACTACAGACTGCCCCAGGGGCCACTGGAGAGACTCCCCCTGTGAGGGCCATCCCCAGGGGGGTACCCCCACTGAGATATATAGGAGAGTACAACAGATGCCCCAGGGGCCAGTTCAGACTACAGATTCCAGGGGGCCCCCCTC ### A CGCAGAGGGAGGCCTTTCCCAGGCGAACTCGAGGGGGGGG   | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTACAGGAGGACGTGTTCTGGAGGACGACGTTTTCTTTACTATAGGAGGACGTTATACGAGGGTGTCTGAGACGACGTTTTCCTTTTTTTT  
   | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGCACGTGTCGCGGCCCAGGGTCAGGGCCCAGGGTATGGGGGACGCCCTATGTTCCTTTACTATGGGGGACGCCTATGTTTTTACGAGGCTTTTTTTT   | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGCACGTGTCGCGGCCCAGGGTCAGGGCCCAGGGTATGGGGGACGCCCTATGTTCCTTTACTATGGGGGACGCCTATGTTTTTACGAGGCTTTTTTTT   | ### ACCCAGAGAGAGACTCCTGAGAGATGGCGTTTAACGACGGTGTCCTGGAGAGAGA  | ### ACCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCCACTGTGCGCGGCCCAGGGTCAATGGGGGACECCAGGTTTGACCTTGACCCTCAGACGACGTTCCTGAAGACGACGTTCTGAGACGACGTTCCTGTGCGCGCGC  | ### ACCCCTGAACTACAGGGTTGAGATGGGGTTTACCGCGGGTGCTGGAGAGGAGGTGTTGTGCCCACTGTGCGCGGCCCAGGGTAATGGGGGACGCCAGGTTTGACCTTGAC  #### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  #### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  #### CTCCCCAGGTTGCGGGGGATATTGGGATAAGGGAGGTTGTGTGTG   | ### ACCCCTGAACTACAGGGTTGAGATGGGGTTTACCGCGGGTGCTGGAGAGGAGGTGTTGTGCCCACTGTGCGCGGCCCAGGGTAATGGGGGACGCCAGGTTTGACCTTGAC  #### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  #### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  #### CTCCCCAGGTTGCGGGGGATATTGGGATAAGGGAGGTTGTGTGTG  
  | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTACAGGAGGACGTGTTCTGGAGGACGACGTTTTCTTTACTATAGGAGGACGTTATACGAGGGTGTCTGAGACGACGTTTTCCTTTTTTTT  | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTACAGGAGGACGTGTTCTGGAGGACGACGTTTTCTTTACTATAGGAGGACGTTATACGAGGGTGTCTGAGACGACGTTTTCCTTTTTTTT  | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTAACGACGGTGTCCTGGAGGCACGTGTCGCGGCCCAGGGTCAGGGCCCAGGGTATGGGGGACGCCCTATGTTCCTTTACTATGGGGGACGCCTATGTTTTTACGAGGCTTTTTTTT   | ### ACCCTGACTACAGGGTTGAGATGGGCGTTTACAGGACGATGTTGTGCCACTGTGCGCGGCCCAGGGTAATGGGGACGCAGGTTTGCCTTGAC  ### A F M P R V P M A F M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M P G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M P G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M P G V L L D L R L N P M R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGCGGCGCGATATTGCGATAAGGCAGCTTAAGGGTGTTGTGAGTGTGAGTTGAGGGGGAGTGAGGTTGAGGTTGAGTTTATACAGGCGTAGATTTGCAGGAGGGGGGGG   | ### A COCCAGAGACATCAGACTTCAGACATCCCTAGAGACGATTCTCCTGGAGACACACTTGCCCGGCCCCAGCGTAATGGGGAAGCCCAGGTATGCCCTTGAC  ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### CTCCTCAGCTTCGCGGCGGATATGCGATAAGGCGGTTAAGGGTTGTCAGTGTGTCTCAGTGTGGGGGATGGGGATGGGGATTGAGGATGTTGAGCAGGCTTAAGGGTTGTCAGTGTTCAGTGTGGGGGATATGCGATATGGGATATGCGATAAGGGGGTTGTCAGTGTTCAGTGTGGGGGGATGGGGATGGGGATGGGGATGAGGTTGAGGATGTGGGGGG  | 480  GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAGAGACGATGTTGTGCCCACTGTGCGCGGCCCCAGGGTAATGGGGAACGCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGATAAGGCAGCTTAAGGGTGTGTCAGTGTGTGT  | 480  61  | ### A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E A E R R I N R Y P L K
L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTCGCGGGGGGATATGCGATATGCGACGACTTTAGGGGGGGG  | ASSOCIACACTACAGGATTACAGGATTACAGCAGTGTCCTGGAAGACGATGTTGTGCCCACTGGGCCCTGGGCCCAGGGTCAGGGAGAGGCCCAGGATTTGCCCTTGAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGCCGCATATTGCCATAAGGCACTTAAGGCTGTTGTGTGTG  | ASSOCIATION ASSOCI | ASSOCIATION ASSOCI | SAGATECTGAACTACAGGGTTGAGGATGACGATGTCCTGGAAGACGATGTTGTGCCCACTGGGCCCAGGGCCAGGGTAATGGGGGACGCCTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCAGTGAGTCTGATGTGAGGTGGGGACGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGAGGAG  | GAGATCCTGAACTACAGGGTTGAGTGAGCGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCCATGGGGGCCCAGGGTCAGGGACGCCAGGTATGCCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTCCAGTGAGTCTGATGTGAGGAGGTGGAGGAGGTTGAGGAG   | GAGATCCTGAACTACAGGGTTGAGTGAGCGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCCATGGGGGCCCAGGGTCAGGGACGCCAGGTATGCCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTCCAGTGAGTCTGATGTGAGGAGGTGGAGGAGGTTGAGGAG   | GAGATCCTGAACTACAGGGTTGAGGATGACGACGGTGTCCTGAAGACGATGTTGTGCCACTGGGGGCCCAGGGTAATGGGGGACGCCATTGCCCTTGACCACGACTATGCGTTAACGACGTTTAACGAGTGTCCATTGACGACGACGTTTAACGAGTGTTCAACGAGTTGGGGGCCAGGGTAATGGGGGACGCCTTAAAGGAGTTGAAGTTGAGAGTTGAGAGTTGAGGTGGAGAGACCAGAACCAGAAGATTGCGATAAGGCAGCTTAAAGGAGTTGAGGTGTGATGTGAGGTGGAGGAGGAGAGAACCAGAAGAACCAGAAGAACCAGAAGA   | GAGATCCTGAACTACAGGGTTGAGGATGACGACGGTGTCCTGAAGACGATGTTGTGCCACTGGGGGCCCAGGGTAATGGGGGACGCCATTGCCCTTGACCACGACTATGCGTTAACGACGTTTAACGAGTGTCCATTGACGACGACGTTTAACGAGTGTTCAACGAGTTGGGGGCCAGGGTAATGGGGGACGCCTTAAAGGAGTTGAAGTTGAGAGTTGAGAGTTGAGGTGGAGAGACCAGAACCAGAAGATTGCGATAAGGCAGCTTAAAGGAGTTGAGGTGTGATGTGAGGTGGAGGAGGAGAGAACCAGAAGAACCAGAAGAACCAGAAGA   | GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGGGCCCAGGGCCCAGGGTAATGGGGGACGCCTTGACCCTTGACCCTTGACCACAGAGGTGTCCTGAAGACGATGTGGAAGACGATGTGGGGCCCAGGGCCCAGGGTAATGGGGGACGCCTTAAGGCAGCTTAAGGGTGTTCCACCCCTCACGCTCCCCAGGGGACGCTTAAGGCAGCTTGAGGCTGCCCCACTGAGGATGGCGACCTGAGGAGGTTGAGGTTGAGGTTGAGGCAGACCCCCCCC  | ### GAGATCCTGAACTACAGGGTTGAGGATGACGATGTCCTGGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCTTGACCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGGTGGTGATGAGGATGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTAGTTTAGCGAG  ### L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  ### Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  ### TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAATGGGGGAGAGCTTTGGGGGCACACCCCCTC  ### L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFM  ### ACCCAGAGGAGGCTTTCCCACCCCTGAGGGAACTTGACCTTGTGGCCTTGTCGACATTGAGGTTGTGGGGGGGG   
  | ### GAGATCCTGAACTACAGGGTTGAGGATGACGATGTCCTGGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCTTGACCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGGTGGTGATGAGGATGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTAGTTTAGCGAG  ### L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  ### Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  ### TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAATGGGGGAGAGCTTTGGGGGCACACCCCCTC  ### L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFM  ### ACCCAGAGGAGGCTTTCCCACCCCTGAGGGAACTTGACCTTGTGGCCTTGTCGACATTGAGGTTGTGGGGGGGG  | GAGATCCIGAACTACAGGGTTGAGATGGCGTTTAACGACGAGTGTCCTGGAAGACGATGTTGTGCCCACTGGGCGCGCCCTCAGGGCCTAATGGGGGACECCATGTGCCCTTGAC E I L N Y R V E M A F N D G V 1 E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTCAGTGAGTG  | ### GAGATCCTGAACTACAGGGTTGAGGATGACGATGTCCTGGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCTTGACCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGGTGGTGATGAGGATGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTAGTTTAGCGAG  ### L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  ### Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  ### TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAATGGGGGAGAGCTTTGGGGGCACACCCCCTC  ### L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFM  ### ACCCAGAGGAGGCTTTCCCACCCCTGAGGGAACTTGACCTTGTGGCCTTGTCGACATTGAGGTTGTGGGGGGGG  | GAGATCCTGAACTACAGGGTTGAGATGGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGTGCCACTGGGCCCAGGGCCCAGGGTAATGGGGGACGCCTTGACCCTTGACCCTTGACCACAGAGGTGTCCTGAAGACGATGTGGAAGACGATGTGGGGCCCAGGGCCCAGGGTAATGGGGGACGCCTTAAGGCAGCTTAAGGGTGTTCCACCCCTCACGCTCCCCAGGGGACGCTTAAGGCAGCTTGAGGCTGCCCCACTGAGGATGGCGACCTGAGGAGGTTGAGGTTGAGGTTGAGGCAGACCCCCCCC  | GAGATCCTGAACTACAGGGTTGAGGTGACGAGGTCCCTGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCATTGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTCAGTGAGTG  | ### A FIND G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCC/CAGC/CCGGSCGGATATGGGGATAGGGAGGTTGAGGGGTTGAGGGGTTGAGGGGTGAGGGGTTGAGGATGGGTTAGAGGAG
   | ### ATTIGACCCTGACCTCATGCTTGAGGGGTTACAGGAGGACGTGTTCTGGAGGACGACGTTTTCTTTACTATAGGAGGACGTTATACGAGGGTGTCTGAGACGACGTTTTCCTTTTTTTT  | GAGATC TEACHTACAGGSTTGAGATGACGATTACACACGGTTTACCACAGACACGTTGTCCTGAAGACAGATTGTGTCCATTGTCCCGGGCCCAGCGTAATGGGGACGCCTTGAACCACGAGATCACGAGATCACTTGAGGGCCAGCCTCAGGGCCAGCCTAAAAAAAA   | GAGATC TEACHTACAGGSTTGAGATGACGATTACACACGGTTTACCACAGACACGTTGTCCTGAAGACAGATTGTGTCCATTGTCCCGGGCCCAGCGTAATGGGGACGCCTTGAACCACGAGATCACGAGATCACTTGAGGGCCAGCCTCAGGGCCAGCCTAAAAAAAA   | GAGATC TEACHTACAGGSTTGAGATGACGATTACACACGGTTTACCACAGACACGTTGTCCTGAAGACAGATTGTGTCCATTGTCCCGGGCCCAGCGTAATGGGGACGCCTTGAACCACGAGATCACGAGATCACTTGAGGGCCAGCCTCAGGGCCAGCCTAAAAAAAA   | ### ATTRACCCTGACTACAGGATTGCAGTTGAGCAGTGCTGCTGCAGAACGAGTGTTGTGCCAGGGCCGGGCCGGCC   |
| GAGATCCTGAACTACAGGGTTGAGATGCGTTTAACGACGGTGTCCTGAAGACGATGTTGTGCCACTGGGGGCCTCGCGGGCCTAGTGGGGACGCCAGGTTACCCCTTE  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L  CTCCTCAGCTTCGCGGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTCCAGTGAGTCTGATGTGAGGTGGGGACGATGAGGGTTGAGGAG   | TAACGACGGTGTCCTGGAAGACGATGTTGTGCCCACTGTGCGCGGCGCTCGCGGGCCCAGCGTAATGGGGGACGCCAGGTATGCCCTTGAC  M D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GCAGCTTAAGGGTGTGCAGTGAGGTGGGGGACTGAGGAGGTTGAGGTTGAGGTTTAACGGCGTAGTTAAGGAGA  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  CSTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAAGAAGGAGGGGGGGG  | ### STATES OF THE PRODUCT OF PROD | 81 GAGATCCTGAACTACAGGGTTGAGATGCGTTTAACGACGGTGTCCTGGAAGACGATGTTGCCCACTGTGCGCGGCCCCGCGGCCCAGCGTAATGGGGACGCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATGCCATAAGGCAGCTTAAGGGTGTGTCAGTGTGTGT   | E L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCICAGCTCCGGGCCGATATTGCGATAGGCACTTAGGGGGTTTTTTGCAGTGGGTTGTGTGTG  | 81 GAGATCCTGAACTACAGGGTTGAAGTGGGGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAAGCACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTAAAGGACGTTTTTTTT  
                    | 81 GAGATCCTGAACTACAGGGTTGAAGTGGGGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAAGCACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTAAAGGACGTTTTTTTT   | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  | 81 GAGATCCTGAACTACAGGGTTGAAGTGGGGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAAGCACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTAAAGGACGTTTTTTTT   | 81 GAGATCCTGAACTACAGGGTTGAAGTGGGGTTTAAGGACGGTGTCTGGAAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTAATGGGGGACGCCAGGGTATGCCCTTGAAGCACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTTAAGGACGTTAAAGGACGTTTTTTTT   | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  
   | ### ACCCAGAGGACCTTGACCTCTGAGGACCTTGAACGACGGTCCTGGAGGACGACGTTTTCCCTTTTTTCCTCTT ### ACCCAGAGGACGCCTTGAACCACCCTCTGAGGCCCACCTTTTTCCCTTGAGGCCACCCTCATCTTTTTTTCCCTCTTTTTTTT  | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  | ### ACCCAGAGGACCTTGACCTCTGAGGACCTTGAACGACGGTCCTGGAGGACGACGTTTTCCCTTTTTTCCTCTT ### ACCCAGAGGACGCCTTGAACCACCCTCTGAGGCCCACCTTTTTCCCTTGAGGCCACCCTCATCTTTTTTTCCCTCTTTTTTTT  | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT   
  | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  | 81 GAGATCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAGACGATGTTGTGCCCAGCGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGACGCCTGAGACGCCTGAGACGCCAGGGTTAACGGGGTTTAACGAGAGTTCTCTGAGGGTTTACCAGGGGTGTTAACGGTGTTTTTACCAGGGGTGTTTTTTTT  | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASE OF THE PROPERTY OF TH | ### BASES OF THE PROPERTY OF T | ### BASES OF THE PROPERTY OF T | ### BASES OF THE PROPERTY OF T | ### BASES OF THE PROPERTY OF T | ### BACETAGE TRANSPORTER AND GENERAL FOR THE FORMANCE AND | GAGATCCTGAACTTGAGGGTTGAGATGACGGTTTACCACGGTGTCCTGGAGACACAGTGTTGTGCCACGGCCCTGGGGGCCAGCGTAATGGGAGACTGCTGAAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L L N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L L N P A V G E  GE A E R R I N R Y P L K L L N P A V G E  TIGAGGGCACACCAGAAGATCCTCCTGTAAGGCAGTTGAGCCTCCCAGGGGGGTACCCCCCACTGAGATATATAAGGAGTGACACAAAAAAAA  | ### BASES OF THE PROPERTY OF T  | GAGATCC TEACCTAGAGGTTGAGATGACGATGTCCTGAGAGACAGATGTTGTGCCACTGAGCCGGGCCCAGCGGCCAGCGTAATGGGAACATCTTGACCTTGAC  E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  GE CTCCTAGACTTCGCCGCGATATTGCCATTAGGCCACTTAGGGTGTTGAGTGAG  | GAGATCCTGAACTTGAGGGTTGAGATGACGGTTTACCACGGTGTCCTGGAGACACAGTGTTGTGCCACGGCCCTGGGGGCCAGCGTAATGGGAGACTGCTGAAC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L L N D T L R I N P H R S I L N L N L K D P T T N L L  GE A E R R I N R Y P L K L L N P A V G E  GE A E R R I N R Y
P L K L L N P A V G E  TIGAGGGCACACCAGAAGATCCTCCTGTAAGGCAGTTGAGCCTCCCAGGGGGGTACCCCCCACTGAGATATATAAGGAGTGACACAAAAAAAA  | ### BACETAGE TRANSPORTER AND GENERAL FOR THE FORMANCE AND | ### ACCCAGAGGACCTTGACCTCTGAGGACCTTGAACGACGGTCCTGGAGGACGACGTTTTCCCTTTTTTCCTCTT ### ACCCAGAGGACGCCTTGAACCACCCTCTGAGGCCCACCTTTTTCCCTTGAGGCCACCCTCATCTTTTTTTCCCTCTTTTTTTT   | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC   | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC  | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC  | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC  | ###
ATTIGACCCTGACCTCATGCTTGAGGGCTTTACCGCGGCTAGCCTGAGGGCTAGGGGCCCAGGGCTCAGGGCCCAGGGCTAGGGGCCCAGGGTATGGCGCTAGGCCTTGACCTCTGAGGGCCCAGGGTTGAGGCGCCCAGGGTATGGGGGACGCCAGGTTGAGGAGGACGCCTGAGGGTTGAGGAGGAGGAGGCAGGTTGAGGGTGTTGAGGGTGAGGAGGAGGAGGAGGAGGA  | ### ATTIGACCCTGACCTCATGCTTGAGGGCTTTACCGCGGCTAGCCTGAGGGCTAGGGGCCCAGGGCTCAGGGCCCAGGGCTAGGGGCCCAGGGTATGGCGCTAGGCCTTGACCTCTGAGGGCCCAGGGTTGAGGCGCCCAGGGTATGGGGGACGCCAGGTTGAGGAGGACGCCTGAGGGTTGAGGAGGAGGAGGCAGGTTGAGGGTGTTGAGGGTGAGGAGGAGGAGGAGGAGGA  | ### ACCCAGAGGACTITCACACCTCTGAGGACCTTGACCTCCAGGGGCTACCCTAGGGGCCCAGGGCCCCAGGGCCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCCAGGGCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCC   | ### ACCCTGAACTACAGGGTTGAGATGGGGTTTAACGACGGTGTCTGGAAGACGATGTTGTGCCCACTGTGCGGGGCCCAGGGTAATGGGGGACGCCAGGTTTGACCTTGAC ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D ### E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L ### CTCCTCAGGCTGCGGGGGATATTGGGGATAGGGGGTTTAAGGGGTTGAGGTTGTGAGGTTGAGGTTGAGGTTGAGGTTAAGGATTGGGGGATATTGGGGGTAAGTGGGGTTAAGGAGTTGAGGTTAAGGAGTTGAGGTTAAGGATTAGGAGTTGAGGTTAAGGATTAGGAGTTAGGGTTAAGGTTAAGGATTAGGAGG  | ### ACCCCTGAACTTCAAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAAAAAGAGATGTTGTGCCCACTGTGCGGGCCCAAGGTAATGGGGACGCCAAGGTATGCCCTTGAACAAAAAGAGTGTTGTGCCACTGTGCGGGGCCCAAGGTAATGGGGACGCCAAGGTATGCCCTTGAAGAAAAAAAGAGTGGTTGAAGAAACCTTCATGAGAAAAAAAA  | ### ACCCCTGAACTTCAAGGGTTGAGATGGGGTTTAACGACGGTGTCCTGGAAAAAGAGATGTTGTGCCCACTGTGCGGGCCCAAGGTAATGGGGACGCCAAGGTATGCCCTTGAACAAAAAGAGTGTTGTGCCACTGTGCGGGGCCCAAGGTAATGGGGACGCCAAGGTATGCCCTTGAAGAAAAAAAGAGTGGTTGTGCAAGAAAAAAAA  
   | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC  | ### ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGCTAGGCCTGCTGAGGGCCAGGGCCCAGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGCGCTTGAGGACGCCAGGGTATGCGCGCGC  | ### ATTIGACCCTGACCTCATGCTTGAGGGCTTTACCGCGGCTAGCCTGAGGGCTAGGGGCCCAGGGCTCAGGGCCCAGGGCTAGGGGCCCAGGGTATGGCGCTAGGCCTTGACCTCTGAGGGCCCAGGGTTGAGGCGCCCAGGGTATGGGGGACGCCAGGTTGAGGAGGACGCCTGAGGGTTGAGGAGGAGGAGGCAGGTTGAGGGTGTTGAGGGTGAGGAGGAGGAGGAGGAGGA  | ### ATTGACCCTGACTTGAGGGCTTTGAGGGGCTTGAGGGGGTGTCCTGGAGAGGAGGTGTTGTGCCCTGGGGGCCCAGGGTCAGGGAGAGCGAGGTTTGTGCCTTGAC  ### A F M P R P M P N D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D D V V P L C A A L A A Q R N G D A R Y A L D  ### A F M D R V I E D T L R I H P H R S I L N L N L K D P T T N L L  ### A F M D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  ### Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  ### A F M D N Q K I L L Y A V M T S Q G G T P T E E Y R K Y N K M A E E Q F G G N A L  ### A COCCAGAGGAGGCCTTCCCCAGCCCCTCTGAGGGGACTTGAGCCCTCTCCCAGGGGGGGTTTCCCAGGGGGGCCCTGGGAGTTGAGGGGCCATCCCCCACCCCTCTGAGGGGGGGG  | ### A COCCAGAGACATCAGACATCCCTATAGACACCATTTTACCACCACTTGCCCACCTCATATAGACACCCCTATTTTTTTACCACCACCTCAGACCTCAACCCCCAACTTCTAACCACC   | ### 361 GAGATCCTGAACTACAGGGTTGACGAGGTGTACAGGAGGTGTCCTGGAGAGACGAGGTTGTGCCCGGGCCCAGGGTGAATGGGGAACGCCAGGTATGCCCTTGAC  ### 1   | ### A F N D G V 1 E D D V V P L C A A L A A Q R N G D A R Y A L D  ### CTCCTCASCTTCGCGGGCGGATTTGGGGGGGGTTTAACGACGGTGTTCTGGAGGACGACGTTCTGATGGGGGCGCGGCGCGGCGGCGCGGGGGGGG  | ### 361 GAGATCCTGAACTACAGGGTTGAGTTGAGCAGCGTTCCTGGAGAGAGA  
  | ASSISTANCE SERVING A FIND G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTICGCGCCGGATTTGCGCTAAGGCACTTAAGGCTGTTTGCAGTGAGTCTGATGTGAGGCTGCGACTGATGAGGTTGAGGTTGAGTTTATCAGGTTGAGTTTGAGTTTATCAGGCTGAGTTGAGTTGAGTTTATCAGGCTTGAGGTGAGAGTGAGAGAGTCCTCC  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  CO TTGAGGGACAACCAGAAGACCTCCCTGTAGCCCCCCACGGGGGGGG  | ASSOCIATION AND A CONTROL OF A  | ASSOCIATION ASSOCI | SAGATECTGAACTACAGGGTTGAGGATGACGATGTCCTGGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCTTTACC  E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCAGTGAGGTGATGTGAGGTGGGGAGGTTGAGGAG  | GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGAAGACGAGTGTTGTGCCACTGGGGCCCAGGGTAATGGGGACGCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTGTCAGTGAGTCTGATGTGAGGTGGGGAGGTTGAGGAG  | GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGAAGACGAGTGTTGTGCCACTGGGGCCCAGGGTAATGGGGACGCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTGTCAGTGAGTCTGATGTGAGGTGGGGAGGTTGAGGAG  | GAGATCCTGAACTACAGGGTTGAGGATGACGACGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGTAATGGGGACGCCAGGTATGCCCTTGACCACGGTTCCTGAAGACGACGATGTTGTGCCACTGTGGCCCGGGCCCAGGGTAATGGGGACGCCAGGTTAGCCCTTGACCACGACGACGACCACACACA   | GAGATCCTGAACTACAGGGTTGAGGATGACGACGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGTAATGGGGACGCCAGGTATGCCCTTGACCACGGTTCCTGAAGACGACGATGTTGTGCCACTGTGGCCCGGGCCCAGGGTAATGGGGACGCCAGGTTAGCCCTTGACCACGACGACGACCACACACA   | GAGATCCTGAACTACAGGGTTGAGGTGACGAGGTGTCCTGAAGACGATGTTGTGCCACTGGGGCCCAGGGTAATGGGGAGGCCAGGTTAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTG   | ### GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGCCAGGGTAATGGGGGACGCCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTTGAGTGGGGAGGGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGGGGGAGTTGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGA   
   | ### GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGCCAGGGTAATGGGGGACGCCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTTGAGTGGGGAGGGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGGGGGAGTTGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGA   | GAGATCCIGAACTACAGGGTTGAGATGGCGTTTAACGACGAGGTCCCTGGAAGACGATGTTGTGCCCAGGGGCCCAGGGCCAGGGTAATGGGGGACGCCTTTACCCTTGACC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTCAGTGAGTTGAGTTGAGTGGGGAGGTTGAGGAG   | ### GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGCCAGGGTAATGGGGGACGCCCTTGAC  ### E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  ### E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  ### CTCCTCAGCTTGGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTTGAGTGGGGAGGGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGAGGTTGAGGTTGAGGTTGAGGTGGCGAGGGGGGAGTTGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGTTGAGGTTGAGGTTGAGGTGGGGGAGGA   | GAGATCCTGAACTACAGGGTTGAGGTGACGAGGTGTCCTGAAGACGATGTTGTGCCACTGGGGCCCAGGGTAATGGGGAGGCCAGGTTAGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTG   | GAGATCCTGAACTACAGGGTTGAGGAGGGGTTCCTGGAAGACGATGTTGTGCCACTGGGGCCCAGGGTAATGGGGACGCCAGGTATGCCCTTGAC E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTGGGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTGTGCAGTGAGGATGGGGACGTGGGGAGGTTGAGGTTGAGGTTGAGGTGGGGAGGTTGAGGTTGAGGTTGAGGTGGGGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGGGGAGGTTGAGGAG   | ### A FIND G V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E D N Q K I L L Y A V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L A AGGREGATION TOCKNESSES TO CONTROL T | ###
ATTIGACCCTGACCTCATGCTTGAGGGCATTAGGGGGTCAGGGGCTAGGGGGCTAGGGGCCCAGGGTATAGGGGGACGCCAGGGTATGCCCTTGAGGGGGCCCAGGGTATGGGGGACGCCAGGGTATGCCCTTGAGGACGCCAGGGTATGGGGGACGCCAGGGTATGGGGGACGCCAGGGTATGGCGGACGCAGGGTATGGGGGACGCCAGGGTATGGGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGGACGCAGGACGAGGACGCAGGACGAGGACGCAGGACGAGGACGCAGGGACGAGGACGCAGGACGAGGACGCAGGACGAGGACGCAGGACGAGGACGCCCTCCAGGGGACACCCAGGACGACACCAGGACGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCAGGACACCCCAGGACACCCAGGACACCCCAGGACACCCAGGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGACACCCCAGGACGAC  | GAGATCC TEACCTAGAGGTTGAGATGACGATGTCCTGAGAGACAGATGTTGTGCCACTGAGCCGGGCCCAGCGGCCAGCGTAATGGGAACATCTTGACCTTGAC  E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  GE CTCCTAGACTTCGCCGCGATATTGCCATTAGGCCACTTAGGGTGTTGAGTGAG  | GAGATCC TEACCTAGAGGTTGAGATGACGATGTCCTGAGAGACAGATGTTGTGCCACTGAGCCGGGCCCAGCGGCCAGCGTAATGGGAACATCTTGACCTTGAC  E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  GE CTCCTAGACTTCGCCGCGATATTGCCATTAGGCCACTTAGGGTGTTGAGTGAG  | GAGATCC TEACCTAGAGGTTGAGATGACGATGTCCTGAGAGACAGATGTTGTGCCACTGAGCCGGGCCCAGCGGCCAGCGTAATGGGAACATCTTGACCTTGAC  E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  GE CTCCTAGACTTCGCCGCGATATTGCCATTAGGCCACTTAGGGTGTTGAGTGAG  | ### ATTRACCCTCACCCCACCCCCCACCCCCCATTTTTCCCTTGAGGCCTACCCGGGGGCTCACGGGCCCACCGCCAGGTTACAGGGGTGTTTTTTTT  |
| E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L  481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGGCACCTTAAGGCTCTGCAGTGAGTCTGATGTGAGGTTGGCGACTGATGAGGTTGAGGAG  | L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CCACCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGCAGTGGCGACTGATGAGGTTGAGGTTGAGGTTGATGTTATCAGGCGTAGTTTGAGCAG  Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  CCTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGAGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATGCGATAAGGCAGCTTAAGGGTGTTGATGTGAGTCTGATGTGAGGTGGGGCACTGAYGAGGTTGAGGATGA  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGCTATTGCCCTAAGGCAGCTTAAGGCTGTTGTCGGTGAGGTTGAGTTGAGGTGAGGTTGAGGTTGAGGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGAGGTTGAGGTTGAGGTAGAGAGAGGTTTGAGGAG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGGGTGTGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGGAGG   | E I L N Y R
V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGCATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGTCTGATGTGAGCTGGCGACTGAAGAGTTGAGGTTGAGTTGAGTTAACTATCAGGCGTAGAATTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTGACGCCGTCATGAGGGGGGGTACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAATGACCAGAGGGGGGGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGCATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGTCTGATGTGAGCTGGCGACTGAAGAGTTGAGGTTGAGTTGAGTTAACTATCAGGCGTAGAATTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTGACGCCGTCATGAGGGGGGGTACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAATGACCAGAGGGGGGGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGCATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGTCTGATGTGAGCTGGCGACTGAAGAGTTGAGGTTGAGTTGAGTTAACTATCAGGCGTAGAATTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTGACGCCGTCATGAGGGGGGGTACCCCCAGGGGGGGTACCCCCACTGAGATATATAGGAAGTGGCGAAGGAGGAGGAGGAGACAGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E E Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N CRES.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGCTAACCTAGGGGGCCGTGCGGGCCGTGGGAGGGGGGGTTAACTGCCATAGGTTTTT  960  1081 AGGGGTGTTTTTCTAAGGACGCCATTTTTCCCTTATTTTCCCTTGTTTATTTTTTTT  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGCATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGTCTGATGTGAGCTGGCGACTGAAGAGTTGAGGTTGAGTTGAGTTAACTATCAGGCGTAGAATTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTGACGCCGTCATGAGGGGGGGTACCCCCAGGGGGGGTACCCCCACTGAGATATATAGGAAGTGGCGAAGGAGGAGGAGGAGACAGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E E Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N CRES.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGCTAACCTAGGGGGCCGTGCGGGCCGTGGGAGGGGGGGTTAACTGCCATAGGTTTTT  960  1081 AGGGGTGTTTTTCTAAGGACGCCATTTTTCCCTTATTTTCCCTTGTTTATTTTTTTT  
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCGTATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGTGCGACTGAAGGTTGAGGTTGAGTTGAGGTTGAGTTGAGGTTAAGGAGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG   
  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCGTATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGTGCGACTGAAGGTTGAGGTTGAGTTGAGGTTGAGTTGAGGTTAAGGAGG   
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAAGATTGAGGTTGAGTTGAGTTAACTATGCAGGGGGACACCGCATATTGAGCAGCGGATATTAAGCAGCTTGAGGTGAGAGTTGAGGTGAGAGTGAGAGTGAGAGTGAGAGTTGAGGTGAGATTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAGAGTTGAGGTTGAGGTGAGAGTGA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAGAGTTGAGGTTGAGGTGAGAGTGA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGCAGCGGGAGTGAGAGTTGAGGTTGAGGTGAGAGTGA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG   
  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGCTTGCAGTGGAGTCTGATGTGAGGAGTTGAGGTTGAGGTTGAGGTTGAGTTGAGGAG   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCACCTTAAGGCTGGAGTCTGATGGGGTGGGGCACTGATGAGGTTGAGTTGAGTTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TGGAGGACAACCGAAAGATCCTCCTGTAGGCCTCCTGAGGGGGGGACCCCCACTGAGATTATAGGAGTTCAACAAGATGGCCGAGGAGCAAGGTGGGGGGAACCCCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E E Y Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRB¹  721 ACGCAGAGGAGGTTTCCCAGGGGGAACTTGACCTCATGGGGCTAACCTAGGGGCCACTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTGCGGGGGGATATTGCGATAAGGCAGCTTAAGGGTTGTGTGGGGTGGGGGTTGTGAGGTGGGGGGGG   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCGCTTAAGGCTTGCAGTGGGTCTCTGTGGGGTGGGGCTGATGAGGTTGAGTTGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TGGGGGACAACCAGAGAGTCCTCCTGTAGGCCTCTGAGGCGGGGTACCCCACTGAGATTATGGAGGTCAACAGAGTGCCGGGGGGGG   
   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCACCTTAAGGCTGGAGTCTGATGGGGTGGGGCACTGATGAGGTTGAGTTGAGTTGAGCAG  C L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TGGAGGACAACCGAAAGATCCTCCTGTAGGCCTCCTGAGGGGGGGACCCCCACTGAGATTATAGGAGTTCAACAAGATGGCCGAGGAGCAAGGTGGGGGGAACCCCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E E Y Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRB¹  721 ACGCAGAGGAGGTTTCCCAGGGGGAACTTGACCTCATGGGGCTAACCTAGGGGCCACTGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCACCTTAAGGCTTGCAGTGGAGTCTGATGTGAGGAGTTGAGGTTGAGGTTGAGGTTGAGTTGAGGAG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGCGTATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGTGCGACTGAAGGTTGAGGTTGAGTTGAGGTTGAGTTGAGGTTAAGGAGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT   
  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GOCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGCGCGCGC  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GOCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGCGCGCGC  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGAGGTGGGGGGCGTGAGGGTTGAGGTTGAGGTTGAGGTTGAGCAGAGTTTAAGGCAGTAGTATTAAGGAGTGTTAAGGTTTAAGGAAGTTTAAGGATCCTCCTAGAGGTTGAGCTTCAGGGGGGGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGAGTGAG   
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGGATATGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGGGTGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGGATATGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGGGTGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GOCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCAGTTGTCAGTGAGTCTGATGTGAGGCGCGCGC  | E I L N Y R V E M A F N D G V L E D O V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  600  CICCTCAGCTTCGCGCGCGCATATTGCGATAAGGCACTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGCTGCAGTGTGAGTTGAGTTAGGCTTGAGTAGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTAGT   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L 
CTCCTCAGCTTCGCGCCGCGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGGTCTGATGTGAGGTGGGCTCATGAGGTTGAGGTTTAAGGCTTGAGTTGAGGTTGAGGTTGAGGTTGAGGTTTAAGGCATGTTTTAAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGGGGAGAGATCTTGGGGGCAACGCCCTT  T Q N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTTTTCCTTGGGTTTTTTCCTTCTTCTTTTTTTT   | E I L N Y R V E H A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGTGGGGCACTGATGAGTTTAAGGCTTAAGTTTAAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGGGGAACAGCCCTTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  ATTGACCCTGACCTCAGCTCTGAGGGCACTTCAACCTCTAGGGCTAACCTAGGGGCAACTTTTTTCCCTCTTAGGTTTTTTTCCTTTTTTTT   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCGATGAGTCTGAGTGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGCATATTGCGATAAGGCACCTTAAGGGTGTTGCAGTGAGTCTGATGTGAGGTTGAGGTTGAGGTTGAGGTTAAGGTTTATCAGGCGTAGTATGAGGAGT  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGGAGTTTGGGGGCAACGCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCTGAGGGAACTTGAACTCTATAGGCCTTGCAGATTTTGGGGGGCCAGGGGGGGG   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTGTGAGTGTGAGTTGAGGTGAGGTGAGGTTGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  1720 TTGAGGGACAACCAGAAGATCCTCCTGTAGCCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTGACACAAGATGAGCAGGAGGAGGTTTGGGGGCAACGCCCCTC  L R D N Q K I L L Y A V M T S Q G G Y P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  1721 ACGCAGAGGGAGCTTTCCCAGCTCCTGAGGGCACTTGAACCTCAGGGCTAACCTAGGGCTTGCGCAGGGGGGGG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGGCGGATATTCCGATAGGCACCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGCTGTGAGTTGAGTTGAGTTAAGGTTGAGTTTATCAGCGGATTTTACAGCGAGTTTTACAGCAGTGTTTACAGCAGTTTTACAGCGAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTTACAGCAGTTTACAGCACTCCCACGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGAGAGTTTGGGGGCAACGCCCCCACTGAGATATATAGGAAGTTACAACAAGATGGCCAAGGAGAGAGA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481
CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGTTTGAGGAG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCCGGATATTGCGATAAGGCAGCTTAAGGGTTGTCAGTGAGTCTGATGTGAGGTTGGCGACTGAYGAGGTTGAGGAACCAGAAGAATGGCCGAACCAGAAGAATGACCAGAAGAATGGCCGAACCAGAAGAATGGCCGAGAGAACCAGAAGAATGGCCGAGAGAACCAGAAGAATGGCCCTCCCCAGGGGGGGAACCCCCCCC   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGGCACCTTAAGGCTGTTGTCAGTGAGTTGTGAGGTTGGGATGCGCGACTGATGAGGTAGAGAGAGAGAGACCCCCCCC  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGGCACCTTAAGGCTGTTGTCAGTGAGTTGTGAGGTTGGGATGCGCGACTGATGAGGTAGAGAGAGAGAGACCCCCCCC  | E I L N Y R V E M A F N B G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGCAGCTTAAGGTCTTGCAGTCTGATGTGAGGTTGAGGAG  | E I L N Y R V E M A F N B G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I H P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGCAGCTTAAGGTCTTGCAGTCTGATGTGAGGTTGAGGAG  | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGCACCTTAAGGTGTTGTCAGTCA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGCACCTTAAGGTTGTCAGTCA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGCACCTTAAGGTTGTCAGTCA                             
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCCGCGATATTCCCATAGCCACTTAAGGCTGTTGCATCAGTCTGTCAGTCTGATGTGCGCACTGATGAGGTGCCGACTGAGGAGGTGAGGTGAGGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGAG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGCACCTTAAGGTTGTCAGTCA   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTGCGATAAGCACCTTAAGGTGTTGTCAGTCA   | E I L N Y R V E M A F N B G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCAGCTTCGCGCGCGGATATTCGGATAGGCACCTTAAGGCTCTTGCAGTCTGATGTTGAGGTGGCGACTGATGAGGTTGAGGTTGAGTTTATCAGGCGTATATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1 TGAGGGCAAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATAAGGAAGATACAAGAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  1 R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  1 R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS  1 Q R R L S Q L L R E L E L Y G L V E I E V Y G R G R G R G V N W H V V P S S S  1 Selement D •  840  1 TTGATGGCCTGACCTCATGCTTGAGGCCATAAGGAGGGCTCACCTGAGGGCTAACCTAGGGGCCAGTTTCTCTGGGGTTTTTTTATGAGCTCCATAGTTTTT  960  1 TTAGTTGGCCTAAGCAGAACTTGAAGGAGGTCCCCCCTTTTTCGCTTATTTTCCCAGGGCCACTTTCTTT   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGACTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAG   
   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  GTCCTCASCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTGCGATGGTGTGTGT  | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCGCTTAAGGCTTGCAGTGGGTCTCTGTGGGGTGGGGCTGATGAGGTTGAGTTGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TGGGGGACAACCAGAGAGTCCTCCTGTAGGCCTCTGAGGCGGGGTACCCCACTGAGATTATGGAGGTCAACAGAGTGCCGGGGGGGG   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCGCTTAAGGCTTGCAGTGGGTCTCTGTGGGGTGGGGCTGATGAGGTTGAGTTGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TGGGGGACAACCAGAGAGTCCTCCTGTAGGCCTCTGAGGCGGGGTACCCCACTGAGATTATGGAGGTCAACAGAGTGCCGGGGGGGG   | E I L N Y R V E N A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P N R S I L N L N L K D P T T N L L  CTCCTCAGCTTCGCGGCGGATATGCGCATAAGGCGCTTAAGGCTTGCAGTGGGTCTCTGTGGGGTGGGGCTGATGAGGTTGAGTTGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L K P A V G E  TGGGGGACAACCAGAGAGTCCTCCTGTAGGCCTCTGAGGCGGGGTACCCCACTGAGATTATGGAGGTCAACAGAGTGCCGGGGGGGG   | E I L N Y R V E M A F N D G V L E D D V V P L C A A L A A Q R N G D A R Y A L D  E E A E R R I N R Y P L K L T N D T L R I N P H R S I L N L N L K D P T T N L L  481 CTCCTCACCTICECGSCCCCATATTCCCATAGGCACCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGCATGGCCACTGATCAGGTTGAGTTTAAGTTTAAGCAGGCTGATTGAGCTGAGTTTAAGTTTAAGCAGGTGTGAGGTTGAGGAACAAGAAGAGTTGAGGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG   |
| 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTCAGTGAGTTGATGTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGC  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G  601 TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGACCAGTTTGGGGGCCACCCCCL  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8:  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACCTCATGGCCTTGTCGAGATTGAGGTTGTCGGCGGGGGGGG   | GCACCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGTTGAGGACTGATGAGGTTGAGGTTTAACGGCGTAGTATTGAGCAG Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E CGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACGCCCTC V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M CMF8' ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGTTAACTGGCCATGTTGTTCCTTCTTCTCT L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D • GAGGTCCCCTTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT ACTTGCAAAAGAGTGGTTGATATTACAGGCTTGTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT ACTTGCAAAAGAGTGGTTGATATTACAGGCTTGCTCTATTTTTGGGTTGGTT   | 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGAGGTGGGATGGGGATGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L H D A P A T P P P N V R H ORF8'  T1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  841 ATTGACCCTGACCTCTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  10 P D L N L E A J R R S L *  11 D P D L N L E A J R R S L *  1200  GAAATTGAGCAATTTAAGGCCAACTATTAAGGGCGCAACTTTTTCGAGGGATTTACAGGATTTTTCGAGGACTTTTTTGGGTTTGGTTTCTTCTACTAAGGTGTTGTTT  10 AGGGGTGTTTTGATGAAATTTAAGGCCAACTATTAAGGGGCTGCTAACAAAAGAGTGTTTAACAGAATTTTTTTT  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTACAGGCGTAGTATTAGACAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGGCGGGGAGAGGCGTTTGGGGGGCAACCCCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H ORF8'  TO Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  E1ement D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTAGACCTCATGGTTTTTT  T Q P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCATTTTTCGCTTAGTTGCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACCTAAGGGTTGTTT  1080 AGGGGTGTTTTGATGGACAATTTTAGACGCCACTTTTTACTACAAAAGAGTTGTTTTTCCCTGCCTATTTTGGGTTGTTTTTTTGGGGGGCAACTCTAAAACTTTTAGACGATGCTCTAAAACTTTTTAGACGCCCAGGTCCTAAAA  0RF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGGGGACACTTTTTTCGACGGGGAAACTTTTTTGAGGACCCAGGTCTCAAGAAGTTTTTTAGAGCCCCTATCTGGCT  1320 GTAGTAGAAACTTTAAGGCAGACTATTAAGGGCGACTTTCTATTTTCGACGGGAAAATTTTAAGGCCCTGAATGATGACGATGCCCTATCTGGCT  1321 GTAGTAGAAACTTTAAGGCAGACTATTAAGGGCGGCTTCTATTTTTTTT   | 481 CTCCTCAGCTTCGCGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTACGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATTGGGGGGAGAGTTTGGGGGGAACGCCCCTC  L R D N Q K I L L Y A V M I S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCATTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGCGCGTGGGAGGGGGTTAACTGCCATGTTTCTCTCTC   | 481
CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M CMF8*  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R R R V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGGCTAACCTAGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M CMF8*  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R R R V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGGCTAACCTAGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GREN  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R R G V N W H V V P S S S  Element D  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAGTTTTTTGCCTGAGGTGTTTTTAAGACTCCATAGGTTTTT  960 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCACCGCCATTTTTCCCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTTGCTGAGGTGACTGCTAAGGTGTTTTT  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCACCGCCATTTTTCCCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTTGCTGAGGTGACTGCTAAGGTGTTTTT  962 T D P D L N L E A J R R S L *  1081 AGGGGTGTTTTTGATGGAATTTAGAGGCCACCGCCATTTTTACTAGAGGTGTTAACATTTTTTTT  | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   
   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GREN  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R R G V N W H V V P S S S  Element D  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAGTTTTTTGCCTGAGGTGTTTTTAAGACTCCATAGGTTTTT  960 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCACCGCCATTTTTCCCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTTGCTGAGGTGACTGCTAAGGTGTTTTT  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCACCGCCATTTTTCCCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTTGCTGAGGTGACTGCTAAGGTGTTTTT  962 T D P D L N L E A J R R S L *  1081 AGGGGTGTTTTTGATGGAATTTAGAGGCCACCGCCATTTTTACTAGAGGTGTTAACATTTTTTTT  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG  
  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG  
   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTA   
  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGATGGAGGATGGAGGTGAGGTTGAGGTTGAGGTTGAGGTTTAAGGTAGTA  | CTCCTCAGCTTCGCGGCGGGTATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTATTTAAGCAGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGACGCGGTACCACCCCAGGGGGTACCCCCAGGGGGTACCCCCAGGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGTGGGGCTAACCTGAGGGCAACTTTCTCTGGGGTGGGAGGGGGGGG  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTA   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | CTCCTCAGCTTCGCGGCGGGTATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTATTTAAGCAGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGACGCGGTACCACCCCAGGGGGTACCCCCAGGGGGTACCCCCAGGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGTGGGGCTAACCTGAGGGCAACTTTCTCTGGGGTGGGAGGGGGGGG   
  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGATGGAGGATGGAGGTGAGGTTGAGGTTGAGGTTGAGGTTTAAGGTAGTA  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   
   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGCGACTGATGAGGTTGAGTTTACAGGCGTAGTATTGAGCAG  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGACGCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCCAGAGGACTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTTATGGAGTTGTCGCGAGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGTGTGAGGTTGAGTGAG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTG  
  | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGAGGTTGAGGTTGAGGTTTACTAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATTATAGGAAGTACAACAAGATGGCGAGGACAACTTTGGGGGCAACGCCCTT  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N GRF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTTGTGGCCTTGTGGGATTGAGGGTTGTCGGCGGGGGGGG  | CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCCAGTGAGTTGAGGATGGGGATGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTTACAGCAGGAGCAGCAGAGAGAG  | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCAGTGAGGTCTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTTGAGCAGGCCTAGTAGTATTTGAGCAGCCCTCAGAGATATTGCGAAGATGAGATGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTAGAGCAGCCCTC  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGCCCGCTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATAAGGAAGTACAAGAATAGCAAGATGGCGAGAGGAGAGAGTTTGGGGGACAACCAGAATAGACAGAATAGGAGAGAGA   | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGATTGA   
   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTTGAGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGATGTGAGCAGACCLAGGCGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGGCGAACGCCCCTC L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  TA AGGCAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGCAGATTCAGGAGTTCTCGCAGGGGCCGTTGGGAGGGGGTTAACTGGCATTTTCCTCCTTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  1081 ATGGCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  1081 AGGGGTGTTTTGATGGAATTTAAGGCCCACCGCCACTTTTTCGCTTATTTTGCCTAGCACCCAGTTCTATAAACTTAATAAGGTAGACTGTTACAGTATCTTTAACTAAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAAGGCCCACCGCCACTTTTTCGCTTATTTTGCCAGCACCAAGAACTTTTTGGGTTTGGGTTTTTTGGGTTGGGTTTTTTTGGGTTGGGTTTT | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATTAGGAAGTACAACAAGATGGCGGAGAGATTTGGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8.  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTCAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTTC  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTGCCTGAGGTTTTTTTT  | 481 CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720 1736 1736 1736 1736 1736 1736 1736 1736  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCGTTGTCAGTGAGTTCTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  11GAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAAGGAGAGTTTGGGGGCAACGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCAGAGGAGGCTTTCCCCAGCTCCTGAGGGAACTCTATGGCCTTGTGCAGATTGAGGTTGGCGGGGGCGGTGGGAGGGGGGTTAACTGCCATGTTTTCTCTCTC   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCGTGAGTCTGATGTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGACAGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFB.  TO R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  10 P D L
N L E A I R R S L **  11 D P D L N L E A I R R S L **  1200  961 TTAGGTTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAGGTTTATCAGGATTTTTGACCTCATAGGTTTTTT  1080  1081 AGGGGTGTTTTGAGGACATTTAGAGGCCATTTTACACAAAAGAGTGGTTGATATTTACAGGCTTCTTTTTTGGGTTGGTT  | 481 CTCCTCAGCTTCGCGCGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTCCAGTGAGTTGAGTTGAGGTGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGCTTGAGCACCAGCCCTAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAACCAGAAGA   | 481 CTCCTCAGCTTCGCGCGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTCCAGTGAGTTGAGTTGAGGTGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGCTTGAGCACCAGCCCTAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAACCAGAAGA   | 481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTAGTTGAGGACGCCTGAGGAGGAGGAGCTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGA  | 481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTAGTTGAGGACGCCTGAGGAGGAGGAGCTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGA  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G I P I E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  S41 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTTCCTGGGTTTTTTGCCTGGATTTTTTGCCTGGATTTTTTTT   | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | 481 CTCCTCAGCTTCGCGCCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTTGAGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG:  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  840  841
ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCTAACCTAGGGGCCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGAATCTGAAGGCCCAATTTTTCGCTTGATTTTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1 ORO ORFIL M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G I P I E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  S41 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTTCCTGGGTTTTTTGCCTGGATTTTTTGCCTGGATTTTTTTT   | 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA*  T1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTCTGGGATTTTTGCCTGGATTTTTTGCCTGTGAGTTTTTTTT  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGGCGAGAGGAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCATTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGCGCGTGGGAGGGGGTTAACTGCCATGTTTCTCTCTC  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  |
CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | 481 CYCCTCAGCCTTCGCGCGGATATTGCGATAAGGCAGCTTAAGGCTGCTTCAGTGAGTG   |
| 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTCAGTGAGTTGATGTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGC  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G  601 TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGACCAGTTTGGGGGCCACCCCCL  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8:  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACCTCATGGCCTTGTCGAGATTGAGGTTGTCGGCGGGGGGGG   | GCACCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGTTGAGGACTGATGAGGTTGAGGTTTAACGGCGTAGTATTGAGCAG Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E CGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACGCCCTC V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M CMF8' ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGTTAACTGGCCATGTTGTTCCTTCTTCTCT L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D • GAGGTCCCCTTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT ACTTGCAAAAGAGTGGTTGATATTACAGGCTTGTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT ACTTGCAAAAGAGTGGTTGATATTACAGGCTTGCTCTATTTTTGGGTTGGTT   | 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGAGGTGGGATGGGGATGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L H D A P A T P P P N V R H ORF8'  T1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  841 ATTGACCCTGACCTCTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  10 P D L N L E A J R R S L *  11 D P D L N L E A J R R S L *  1200  GAAATTGAGCAATTTAAGGCCAACTATTAAGGGCGCAACTTTTTCGAGGGATTTACAGGATTTTTCGAGGACTTTTTTGGGTTTGGTTTCTTCTACTAAGGTGTTGTTT  10 AGGGGTGTTTTGATGAAATTTAAGGCCAACTATTAAGGGGCTGCTAACAAAAGAGTGTTTAACAGAATTTTTTTT  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTACAGGCGTAGTATTAGACAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGGCGGGGAGAGGCGTTTGGGGGGCAACCCCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H ORF8'  TO Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  E1ement D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTAGACCTCATGGTTTTTT  T Q P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCATTTTTCGCTTAGTTGCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACCTAAGGGTTGTTT  1080 AGGGGTGTTTTGATGGACAATTTTAGACGCCACTTTTTACTACAAAAGAGTTGTTTTTCCCTGCCTATTTTGGGTTGTTTTTTTGGGGGGCAACTCTAAAACTTTTAGACGATGCTCTAAAACTTTTTAGACGCCCAGGTCCTAAAA  0RF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGGGGACACTTTTTTCGACGGGGAAACTTTTTTGAGGACCCAGGTCTCAAGAAGTTTTTTAGAGCCCCTATCTGGCT  1320 GTAGTAGAAACTTTAAGGCAGACTATTAAGGGCGACTTTCTATTTTCGACGGGAAAATTTTAAGGCCCTGAATGATGACGATGCCCTATCTGGCT  1321 GTAGTAGAAACTTTAAGGCAGACTATTAAGGGCGGCTTCTATTTTTTTT   | 481 CTCCTCAGCTTCGCGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTACGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATTGGGGGGAGAGTTTGGGGGGAACGCCCCTC  L R D N Q K I L L Y A V M I S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCATTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGCGCGTGGGAGGGGGTTAACTGCCATGTTTCTCTCTC   | 481
CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGCTCCTCTTTTTTGGCAGGGGAACTTGCCCCAGGGGCAACTTTTGCCTGGAGGTTGTGGGGTTGTCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGTGTGAGGTTGGGGACTGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGTATTTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCTCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACCCCCTTGTACAGCTCCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCACACCCCCTGTAGAGCACTCCCCCTGTAGAGCACTCCCCCCTGTAGAGACTATATAGGAATTAGGAAGTACAACAAGATGGCCGAGGGGGGGAACCTTCCCCTGTAGAGACTCCCCCTCTGAGGGACTTGAACCTCATGGCCTTGCGAGATTGAGGTTTGCGGCGGGGGGGG   
   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCCTCTTGGGGGCAACCTCCTGTAGAGACTCCCCTGTAGAGACTACAAGAAGTATATAGGAAGTACAACAAGATGGCCGAGGAGCAGGCAG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCCTCTTGGGGGCAACCTCCTGTAGAGACTCCCCTGTAGAGACTACAAGAAGTATATAGGAAGTACAACAAGATGGCCGAGGAGCAGGCAG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGACGTATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCCTCTTGGGGGCAACCTCCTGTAGAGACTCCCCTGTAGAGACTACAAGAAGTATATAGGAAGTACAACAAGATGGCCGAGGAGCAGGCAG   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG   
  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG  
   | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 2 CTCCTCABCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGATGAGGTTGAGGTTTAGAGTATATTGAGCAGG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TGAGGACACCAGAAGATCCTCCTGTACGCCTCATGAGCTCCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC TAGAGGAATATATAGGAAGTACAACAAGATGGCGAGGAGCAGCTCTCCTCTTAGAGGACTCCCCCAGGGGAACATATATAGGAAGTACAACAAGATGGCGAGGAGCAGGCAG  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTA   
  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGATGGAGGATGGAGGTGAGGTTGAGGTTGAGGTTGAGGTTTAAGGTAGTA  | CTCCTCAGCTTCGCGGCGGGTATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTATTTAAGCAGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGACGCGGTACCACCCCAGGGGGTACCCCCAGGGGGTACCCCCAGGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGTGGGGCTAACCTGAGGGCAACTTTCTCTGGGGTGGGAGGGGGGGG  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTA   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | CTCCTCAGCTTCGCGGCGGGTATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTCTGATGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTATTTAAGCAGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGACGCGGTACCACCCCAGGGGGTACCCCCAGGGGGTACCCCCAGGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M M V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGTGGGGCTAACCTGAGGGCAACTTTCTCTGGGGTGGGAGGGGGGGG   
  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGATGGAGGATGGAGGTGAGGTTGAGGTTGAGGTTGAGGTTTAAGGTAGTA  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTCGTGAGGTTGAGGATGAGGTTGAGGTTGAGGTTTACCAGGCGTAGTATGAGCAG  C L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGCACAACCAGAAGATCCTCCTGTACGCCTCTAGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGCAGTTTGGGGGCAACGCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  ACGCAGAGGAGGCTTTCCCAGCCCCTCTGAGGGACTTGACCTTGTCGAGATTGAGGTTGTCGGCCTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   
   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGCGACTGATGAGGTTGAGTTTACAGGCGTAGTATTGAGCAG  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGACGCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCCAGAGGACTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTTATGGAGTTGTCGCGAGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGTGTGAGGTTGAGTGAG   | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTG  
  | 481 CTCCTCAGCTTCGCGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | 481 CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGGGGACTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGAGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E TTGAGGGACACCAGAAGATCCTCCTGTACGCCTCTAGACCCCCCCC   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTCTGATGTGAGGATGAGGTTGAGGTTGAGGTTTACTAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATTATAGGAAGTACAACAAGATGGCGAGGACAACTTTGGGGGCAACGCCCTT  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N GRF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTTGTGGCCTTGTGGGATTGAGGGTTGTCGGCGGGGGGGG  | CTCCTCAGCTTCGCGGGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCCAGTGAGTTGAGGATGGGGATGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTTACAGCAGGAGCAGCAGAGAGAG  | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCAGTGAGGTCTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTTGAGCAGGCCTAGTAGTATTTGAGCAGCCCTCAGAGATATTGCGAAGATGAGATGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTAGAGCAGCCCTC  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGCCCGCTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATAAGGAAGTACAAGAATAGCAAGATGGCGAGAGGAGAGAGTTTGGGGGACAACCAGAATAGACAGAATAGGAGAGAGA   | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGATTGA   
   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTTGAGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGATGTGAGCAGACCLAGGCGTAGTATTGAGCAG 600 L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGGCGAACGCCCCTC L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  TA AGGCAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGCAGATTCAGGAGTTCTCGCAGGGGCCGTTGGGAGGGGGTTAACTGGCATTTTCCTCCTTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  1081 ATGGCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  1081 AGGGGTGTTTTGATGGAATTTAAGGCCCACCGCCACTTTTTCGCTTATTTTGCCTAGCACCCAGTTCTATAAACTTAATAAGGTAGACTGTTACAGTATCTTTAACTAAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAAGGCCCACCGCCACTTTTTCGCTTATTTTGCCAGCACCAAGAACTTTTTGGGTTTGGGTTTTTTGGGTTGGGTTTTTTTGGGTTGGGTTTT | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATTAGGAAGTACAACAAGATGGCGGAGAGATTTGGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8.  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTCAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTTC  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTGCCTGAGGTTTTTTTT  | 481 CTCCTCAGCTTCGCGSCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720 1736 1736 1736 1736 1736 1736 1736 1736  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGCGTTGTCAGTGAGTTCTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  11GAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAAGGAGAGTTTGGGGGCAACGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCAGAGGAGGCTTTCCCCAGCTCCTGAGGGAACTCTATGGCCTTGTGCAGATTGAGGTTGGCGGGGGCGGTGGGAGGGGGGTTAACTGCCATGTTTTCTCTCTC   | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGCGTGAGTCTGATGTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGACAGCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFB.  TO R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  10 P D L
N L E A I R R S L **  11 D P D L N L E A I R R S L **  1200  961 TTAGGTTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAGGTTTATCAGGATTTTTGACCTCATAGGTTTTTT  1080  1081 AGGGGTGTTTTGAGGACATTTAGAGGCCATTTTACACAAAAGAGTGGTTGATATTTACAGGCTTCTTTTTTGGGTTGGTT  | 481 CTCCTCAGCTTCGCGCGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTCCAGTGAGTTGAGTTGAGGTGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGCTTGAGCACCAGCCCTAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAACCAGAAGA   | 481 CTCCTCAGCTTCGCGCGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTCCAGTGAGTTGAGTTGAGGTGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGCTTGAGCACCAGCCCTAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAGCACCAGAACCAGAAGA   | 481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTAGTTGAGGACGCCTGAGGAGGAGGAGCTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGA  | 481 CTCCTCAGCTTCGCGCGCGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTAGTTGAGGACGCCTGAGGAGGAGGAGCTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGA  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G I P I E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  S41 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTTCCTGGGTTTTTTGCCTGGATTTTTTGCCTGGATTTTTTTT   | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | 481 CTCCTCAGCTTCGCGCCGGATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTTGAGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG:  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  840  841
ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCTAACCTAGGGGCCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGAATCTGAAGGCCCAATTTTTCGCTTGATTTTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1 ORO ORFIL M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGAGATGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGCCGCGACGCACTGAGGAGGTGGCGACTGAGGAGGTTGAGGTTGAGGTTGAGGTTGAGGAGGACCTGAGGAGGAGGAGCACTTGAGGAGTTGAGGAGGTGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  | CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTAGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G I P I E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFG.  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  S41 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTTCCTGGGTTTTTTGCCTGGATTTTTTGCCTGGATTTTTTTT   | 481 CTCCTCAGCTTCGCGCGGGATATTGCGATAAGGCAGCTTAAGGCTGTTGCAGTGTGAGTTGAGGTGGCGACTGATGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M I S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA*  T1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCCCTGAGGCCAACCTTCTCTGGGATTTTTGCCTGGATTTTTTGCCTGTGAGTTTTTTTT  | 481 CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTAAGGGTGTTGTCAGTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTTATCAGGCGTAGTATTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGGCGAGAGGAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCATTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGCGCGTGGGAGGGGGTTAACTGCCATGTTTCTCTCTC  | 481 CTCCTCAGCTTCGCGGCGCATATTGCGATAAGGCAGCTTAAGGCTGTTGTCAGTGAGTCTGTGTGAGGTTGAGGTTGAGGTTGAGTTTATCAGGCGTAGTATGATGTTGAGCAG  L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGGAGAGCAGTTTGGGGGCAACGCCCTC  R L P D K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GRF8'  721 ACGCGGAGGGGCTTTCCCAGCGGGGAACTTGACCTCTGGGCCTTGTGCAGATTGAGGGTTGTGGGGGGGG   | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  |
CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | CTCCTCAGCTTCGCGGCGGATATTGCGATAAGGCAGCTTTAAGGCTGTTGTCAGTGAGGTTGTAGTGAGGATGGCGGACTGATGAGGTTGAGGTTGAGGTTTAAGGTTTATCAGGCGTAGTATTGAGCAGG CL L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACAACCAGAAGATCCTCCTGAGCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M GMF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N M H V V P S S S  Element D .  840  841  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTGAGGGCAACTTTCTCTGGGTTTTTTGCTGTAGGGGGGGG  | 481 CYCCTCAGCCTTCGCGCGGATATTGCGATAAGGCAGCTTAAGGCTGCTTCAGTGAGTG   |
| L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G  601 TIGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGATACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCC L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S  841 ATTGACCCTGACCTCATGCTTGAGGCCTATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCCAACTTTCTCTGGATTTTTGCCTTAGTGGAACTCCCTATTTTTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTG  10 P D L N L E A I R R S L **  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTG  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCGCCACTTTTTCGCTTATTTGCCAAGAGCTTCCCCTATTTTTTTGGTTGG  | Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E CSTCATGACCTCCCAGGGGGTACCCCACTGAGATATATAGGAAGTACAACAGATGGCCGAGGAGCACTTTGGGGGCAACGCCCTC V M T S Q G G T P T E L Y R K Y N K H A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M ORF8' ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCGAGGGGCCGTGGGAGGGGGTTAACTGCCATGTTGTTCCTTCTCTT L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D .  GAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  R S L *  CACCGCCATTTTTCCCTTGTGATATTACAGGATTCTTATAACTTATAACTTATAAGGATGACTGTTACAGGTATCTTTACCTAAGGGTGTTGTT  TACTACAAAAGAGTGGTTGATATTACAGGCTACTTGGGTTGGTT  | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGGGGGGTACCCCCACTGAGATATATAGAATAGAAGATGGCGGGGAAACCCCCTC  TGAGGGAAACCAGAAGATCCTCCTGTAGGCGTCATGACCCCCCACTGGGGGGTACCCCCACTGGAGATATAGGAAGTACAACAAGATGGCGGAGAGAGA   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSCTCATGACCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAAAAATGGCCGAAGACACCCCTC  CRDNQKILLYAVMISQGGTCTTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAAAAATGGCCGAGGGAACACCAGAAGATTTGGGGGCAACCCCCCTC  RLPPKGLEQPFKFEIAKDLNLHDAAPATPPPNVRMAEEQFFGGAACTTTGCCTCTTGCGGGATTCATGGCCTTGCCAGGGGGCCGTGGGAGGGGGGGG   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLACCTCCCGGGGGGTACCCCCATTATATAGGAGTACAACAAAATGGCGGGGACAACCCCCTC  QPVVLLDEQVGDNGGGCACAACCAAAACAACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAAATGGCCGAGGACACTTTTTGGGGGCAACCCCCCTC  LRDNQKILLYAVNTSQGGTPTECCAGCCTCCTACGCCGTCAGGCGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAAAATGGCCGGGACAACCCCCCTC  RLPPKGLEQPFKFEIAKDLNDAPTEIYRKYNKMAEEQFFGGAACTTTGGCCTTGTCCGCAGGATTGAACTTGCGCAGGGCCGTGGGAAGGGGGGGTTAACCTGAGGACATGTTCTTCCTCT  RLPPKGLEQPFKFEIAKDLNDAPTTGGCACTCTCTAGGCCTTGTCCAGAATTGAAGTTGTTCGCCTGGCGGCCGTGGGAAGGGGGGGTTAACTGCCATGTTTTTCTCTCTC  | L L S F A A
D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720 | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720 | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q Y G D N G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1720 
1720   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSGGGTACCCCCACGAGAGATATATAGGAGTACAAGAGAGAG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG   
  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGCCCTCTGAGGCACTTGAGGCTGAGATTGAGGCTGGGGGGGG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGGCTCCTGAGGACTTGAGGCTTGTCGAGATTGAGGTTGTCGGGAGGGGGGGTTAACCGCAGAGAGATGTTGGGGGGAGGGGGTTAACTGGCAGAGGAGGCGTTCCCCTTTTTTGCCTGAGATTTTTGCCTGAGTTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGGGTTGTTTCTTTTTTTT  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSGGGTACCCCCACGAGAGATATATAGGAGTACAAGAGAGAG  
   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGGCTCCTGAGGACTTGAGGCTTGTCGAGATTGAGGTTGTCGGGAGGGGGGGTTAACCGCAGAGAGATGTTGGGGGGAGGGGGTTAACTGGCAGAGGAGGCGTTCCCCTTTTTTGCCTGAGATTTTTGCCTGAGTTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGGGTTGTTTCTTTTTTTT  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGGCTCCTGAGGACTTGAGGCTTGTCGAGATTGAGGTTGTCGGGAGGGGGGGTTAACCGCAGAGAGATGTTGGGGGGAGGGGGTTAACTGGCAGAGGAGGCGTTCCCCTTTTTTGCCTGAGATTTTTGCCTGAGTTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGGGTTGTTTCTTTTTTTT  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGGCTCCTGAGGACTTGAGGCTTGTCGAGATTGAGGTTGTCGGGAGGGGGGGTTAACCGCAGAGAGATGTTGGGGGGAGGGGGTTAACTGGCAGAGGAGGCGTTCCCCTTTTTTGCCTGAGATTTTTGCCTGAGTTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGGGTTGTTTCTTTTTTTT  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSSLYIPLVVLHGLLKRPAVGE 601 TTGAGGGACAACCAGAAGATCCTCCTGACCCCGTCAGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGAGACAGTTTGGGGGCAACCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKHAEEQFGGAACAGCCCTC TOUR ON QKILLYAVMTSQGGTYTTCCAGGCTCCTGAGGACTTGAGGCTTGTCGAGATTGAGGTTGTCGGGAGGGGGGGTTAACCGCAGAGAGATGTTGGGGGGAGGGGGTTAACTGGCAGAGGAGGCGTTCCCCTTTTTTGCCTGAGATTTTTGCCTGAGTTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTGGGTTGTTTCTTTTTTTT  | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC  
  | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   
   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLRTGAGGGGGGAACCCCCCAGGGGGGGGACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCACTGAGGACCACCAGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLRTGAGGGGGTACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAAAAAATTGGGAAGATTGGGGGAAACACCAGAAGATCCTCCTGAGGCCCTCCCAGGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAAAATGGCCGAAGGATCCTCCTGAGGGACAACCCCCCACTGAGATATATAGGAAGTACAACAAAAATGGCCGAAGGACGCCCCCCCC   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1760 TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCACTGTACCTCCTGTACCCCCCCC  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKAGUCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACACCCCCCCC   
   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLRTGAGGGGGTACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAAAAAATTGGGAAGATTGGGGGAAACACCAGAAGATCCTCCTGAGGCCCTCCCAGGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAAAATGGCCGAAGGATCCTCCTGAGGGACAACCCCCCACTGAGATATATAGGAAGTACAACAAAAATGGCCGAAGGACGCCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLRTGAGGGGGGAACCCCCCAGGGGGGGGACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCACTGAGGACCACCAGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACAACCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSGGGTACCCCCACGAGAGATATATAGGAGTACAAGAGAGAG   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA   
  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGGGGGGTACCCCCACGGAGATATATAGGAGTACAACAACAACATGGCGGGGACAACCCCCCTCTGGAGACCCCCCCC  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGGGGGGTACCCCCACGGAGATATATAGGAGTACAACAACAACATGGCGGGGACAACCCCCCTCTGGAGACCCCCCCC  | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGGGGGTACCCCATGACATATATAGAAGTACAAAAAAGTTGGGAGACAACAAGAATCCCCTCTTACCCCTATGACCCCCCACGGGGGGTACCCCCACTGACATATATAGGAAGTACAACAAGAATCCCCATGAGACACCCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFFGRAACAAGATTGGGGGGAACAACAAGAAGTACAACAAGAACAAC   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGAGCCCGCTCAGGCGGGGTACCCCCACTGAGATATATAGGAAGTACAAGATGCCGGGGAGAGCAGTTTGGGGGCAACCCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGGAGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTAGTGAACTCCTATTTTTTATGACCTCATAGTTTTT  960  1001 AGGGGTGTTTTGGCTAGAGGGCTGCCCACCGCCATTTTTCGCTTAGTTGCCTAGGGGCCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1002 D L N L E A I R R S L *  1201 GAAATTGATGAGAATTTAAGGCCACTTTTACTACAAAAGAGTGGTTCAATATTACAGGACTTTTTGAGGACCATGCAAGAGTACCTAGAATCCTAAA  1202
GAAATTGATGAGAATTTAAGAGCACATTTTAGGGGCAACTTTTTCGCTAGGGGTTTTTTTGAGGACCATGCTACATGCACCTGAATGACCCTATCTGCT  1203 GAAATTGATGAGAATTTAAGGCACATTTTAGGGGCACCTTTTTTCGACAGGGGTTTTTTCGACGGGGATTTTTTGAGGACCATGCTACAAGAGATGCCCTATCTGCT  1204 GAAATTGATGAGAACTTTAAGAGCACATTTTAGGGGCACCTTTTTTCGACGGGGATTTTTTTT   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAGGTCAACAGAGAGAG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLACCCCCAGGGGGGTACCCCCACTGAGATATATAGGAGGTCAACAGAGAGAG  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGGGGGGTACCCCCACGGAGATATATAGGAGTACAACAACAACATGGCGGGGACAACCCCCCTCTGGAGACCCCCCCC  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGAGAGGGGTTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M QRF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTGTAACTCTATGGCCTYGTCAGAATTGAGGTTGTCGGCAGGGGGCCGTGGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCC   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  601
TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGATGGCCGGAGGAGCAGTTTGGGGGCAACCCCCCTC LRDNQKILLYAVMTSQGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGGAGGAGCAGCCCCTC  720 RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFFGGAACTGTCCTCTCTCCTCT 1 QRRLSQLLRELELYGLVEILEVVGRGGCTGCGGAGGGGGGGTTAACTGGCATTTTCCTCTCTCT 1 QRRLSQLLRELELYGLVEILEVVGRGGCAACTTTTTCCTCTCTTCCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTTATAGCCTCATAGTTTTT  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCCTGAGGGCCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTTATAGCCTCATAGTTTTT  960  1 OPDLNLEAIRRSCAATTCTAAAAGAGGGTCCCCCTTATTTTCCCTATATAACTTATATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGAAATTTAAGGGCACCACCATTTTTCCCTTATATACAGGATTTTTTGGGTTGGTT   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDNGGLPTGGSCTCATGACCTCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCCGAGGAACCAGAAGACCCCCCCC   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGATGGCGGGAGAGCAGTTTGGGGGCAACGCCCTC  TRAD N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR*  721 ACGCAGAGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGGGGGGGG  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGGGAGAGGATGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCTGAGGGAACTGAACT   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSCCTATGACCTCCAGGGGGTACCCCACTGAGATATATAGGAAGTACAACAAGATGACCAGGAGAGACACCCTC  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGACCAGGAGAGAGA   | Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TIGAGGGACACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGATACAACAAGATGGCGAGGAGAGGCGTTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G B N A L  R L P
P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFB*  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGACCTCAACGCCTTGTCGAGATTGAGGTTGCGGCAGGGGCGGGGGGGG   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGATACAAGAAGATGGCGGAGGGACCAGTTTGGGGGCAACCCCCTC  R D N Q K I L L Y A V M T S Q G G T P T E L Y R K Y N K M A E E Q F G B N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS*  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D F  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATAGACCTCATAGTTTTT  960  1 D P D L N L E A J R R S L **  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCCACTTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTCTGAAGGGCCTGCACCGCCATTTTTCGCTTGATTTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1082 AGGGGTGTTTTGATGGAATTTAAGGCCAATTTACACAAAAGATGGTTGATATTACAGGATTTTTTGGGTTGGTT | Q P V V L L D E Q Y G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGCCCCCCCGGGGGGTACCCCCACTGAGATATATAGGAAGAGATAGAGAGAG   | Q P V V L L D E Q Y G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGCCCCCCCGGGGGGTACCCCCACTGAGATATATAGGAAGAGATAGAGAGAG   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSCTCATGACCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSCTCATGACCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1 TGAGGGACAACAGAAGATCCTCCTGTAGGCCGTCATGACCCCCCACTGAGATATATAGGAAGTACAACAGATGGCCGAGAGAGA  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCGGAGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR*  721 ACGCAGAGGAGGGTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGGCGGGGGGGG   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGAAGATGGCGGAGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G
L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR*  721 ACGCAGAGGAGGGTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGGCGGGGGGGG   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  TTGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR*  721 ACGCGAGAGGAGGTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGGCGGGGGGGG  | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  TTGAGGGACAACAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR*  721 ACGCAGAGGAGGGTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGGCGGGGGGGG   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D H G G L P T G G S L Y I P L V V L H G L L L K P A V G E  1 TGAGGGACAACAGAAGATCCTCCTGTAGGCCGTCATGACCCCCCACTGAGATATATAGGAAGTACAACAGATGGCCGAGAGAGA  | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSCTCATGACCCCCCCCGGGGGTACCCCCACTGAGATATATGGAAGTACAAGAAGAGGCGAGTTTGGGGGCAACCCCCCT  TGAGGGACAACCAGAAGATCCTCCTGTAGGCCTCCTCCAGGGGGGTACCCCCACTGAGATATATGGAAGTACAACAAGATGGCCGAGGAGAGAGA   | L L S F A A D I A I R Q L K G V V S E S D V R N A T D E V E V E F I R R S I E Q  Q P V V L L D E Q V G D N G G L P T G G S L Y I P L V V L N G L L L K P A V G E  1 TTGAGGGACAACCAGAAGATCCTCCTGAGGCCGTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAGATGCCGAGGAGAGCAGCCCCCC  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G 8 N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  121 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTGAGCTTGAGGCTTGTCGAGGATTGAGGTTGTTGCGCAGGGGCGGTGGGAGGGGGGTTAACTGCATGTTTTCTCTCTC  
   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQV6DHGGLPTGGSGGGTACCCCCACTGAGATATATAGGAGTACAAGAGAGAGA  | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKAGUCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACACCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKAGUCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACACCCCCCCC   | ULSFAADIAIRQLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKGVVSESDVRNATDEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLKAGUCGCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGACACCCCCCCC   | LLSFAADIAIRQLKGVVSESDVRNATDEVEVEVEFIRRSIEQ  QPVVLLDEQVGDHGGLPTGGSSGTACCCCACTGAGATATATAGGAAGTACAAGAATTAGGAAGTACAAGAAGATTAGGAAGAACCCCCCCC  |
| 601 TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCACCTTTTGGGGGCACCCCCCL L R D N Q K I L L Y A V M T S Q G G T P T E T Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M QRF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGCGCGAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTTCTCTT  | CSTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M CMF8' ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTTGTCTCTCTC   | Transparacy of the properties  | COLUMN TO A CAGAGAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACGCCCTC  LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTTETYRKYNKMAEEQFGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGACCTTCCCAGCTCCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGTTGTGGGGGGGG   | Transgrandaraccaragaractcctctgacccccactgacctccccactgaccatatatat  | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   
                 | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   | Transgraftalagaarattalagaarattalagaarattalagaarattalagaaratalagaaratalagaaratalagaarat | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   |
Transgraftalagaarattalagaarattalagaarattalagaarattalagaaratalagaaratalagaaratalagaarat | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctctct   | Transgraftalagaarattalagaarattalagaarattalagaarattalagaaratalagaaratalagaaratalagaarat | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   
   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctctct  
  | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGACGTTTGGGGGGCAACCCCTC  LRONQKILLYAVNTSQGGTPTETYRKYNKMAAEEQFGGNAACCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRHOMER*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTTGACGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCAACTTGCTGAGGTTGTCCGCAGGGGCCAGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   
   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCCC  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGGGAGAGGAGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVNTSQGGTPTEIYRKYNKHALEQFGGGAGGGGGAGTTTGGGGGCAACCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKHALEQFGGGGAGGGGGGAGTTTCTCTCTCTCT  ACGCAGAGGAGGAGTTCCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGGAGGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGACGTTTGGGGGGCAACCCCTC  LRONQKILLYAVNTSQGGTPTETYRKYNKMAAEEQFGGNAACCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRHOMER*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTTGACGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCAACTTGCTGAGGTTGTCCGCAGGGGCCAGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACCTCATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGGGAGAGGAGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVNTSQGGTPTEIYRKYNKHALEQFGGGAGGGGGAGTTTGGGGGCAACCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKHALEQFGGGGAGGGGGGAGTTTCTCTCTCTCT  ACGCAGAGGAGGAGTTCCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGGAGGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   
   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCCC  | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctccccccactgagatatatat  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT   | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT   
  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFG6NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGE6'  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCAGATTGAGGTTGCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCTCCTCTT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCAGAATTGAGGTTGCGCGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTCTCCTCTT  TQRRLSQLLRELELYGLVEIVGRACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATAGACCTCATAGTTTTT  P60  ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTTATGACCTCATAGTTTTT  AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACAGGGTTGTTT  AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGTTATATAACTTATATAAGGATGACTGTCAGAGTACCTTAAA  1080  AGGGGTGTTTTGATGAGAATTTAGAGGCCTACCAAAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGGTTGGTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACCCCTCTCTCT   | Transpagacian Correspondence Contragacio Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Conservati | Transpagacian Correspondence Contragacio Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Conservati | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC 
RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCCATTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RL P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCTCTTT  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGAGGTTGTCGGCAGGGGCCGTGGGGAGGGGGGTTAACTGGCATTGTTCTTCTCTCTTTTTAGACCTCATAGTTTTT  B40  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  AGGGGTGTTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTCGCTTGATTTTGCCAGAGCCATTTTTGCGTTGGTTTTTTTGGGTGGG  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCATTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKMAEEQFGGAGCATTTGGGGGCAACCCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAACCTCATGGCCTTGTGGGGAACTTGAGGTTGTCGGGGGGGG  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFG6NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGCGCGAGGGGCCGTGGGAGGGGGGTTAACTGGCCTTGTCCTCTCTCT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGAACTTTGGGGGCAACCCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGAACTTTGGGCTTGCTCTCTCTCT RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGGGCTTGCTCTCTCTCTCT ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCGGGGGGGG   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTEIYRKYNKMAEEQFGGAACTTTGGGGGCAACCCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGAGCTTGGGGAGGAGCTTCTCTCTCTCT  RLPPKGLEQPFKFEIAKDLNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  | Tragaggacaaccagaagatcctcctgtacgccgtcatgaggggtacccccactgagatatataggaagtaccaaagatggccaaagataccccactgagatatataggagtaccaaagatggccaaagataccaaaataggccctc to be rong reference by reference refe | TIGAGGGACAACCAGAAGATCCTCGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGGTPTEEYRKYNKMAEEQFGGGTACCCCACTGAGATATATAGGAAGTACAAAAAGAGGTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEYYRKYNKMAEEQFGGAACTGTGGGCAGGGCACTTCTCCTCT  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT  TQRRLSQLLRELFLYGLVFGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGGTGAACTCCCTATTTTTTAGACCTCATAGTTTTT  P60  1 OPDLNLEAIR RSL*  1080 
AGGGGTGTTTTCATGGAACTCTGAAGGGCTGCCCACCGCCATTTTTCCCTTATTTTCCTAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  AGGGGTGTTTTCATGGAATTTAGACGCCATTTTACTACAAAAAACTGTTGTATATTTTCCAGGCCAGTTCTATTTTTTGGTGGCTGCTGACGGCCATGCCAAACACATCCTAAA  1200  BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGGAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCCTGAATGATGACGATGCCCTAACTGCCCTATCTGCT  1320  BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGCAACTTTTTCGACGGGAATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320  BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGCAACTTTTTCGACGGGAATTTACCAAAGAAGTTTTTGAGGACCCTTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320   | TIGAGGGACACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCGAGAGAGA   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKMAEEQFGGACTTTGGGGGCAACCCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGGAGGGGCATTTCTCTCTCT  ACGCAGAGGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCTGCAGGTTGTCGGCGCGGGGGGGG   | Transparacionacionacionacionacionacionacionacion  | Transparacionacionacionacionacionacionacionacion  | Transgrandalcagaagatctcctgtacgccstcatgacctcccagggggtacccccactgagatatataggaagtacaacaagatggccgaggagcagtttgggggcaaccccctct  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA'  To R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCTGAGGGCATAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACCTTCCTGGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960 I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCCCTTTTTCCCTTATTTTCCCTAGGGTGTTTTTTGGCTTGGGTTTTTTTGGGTTGGTT   | Transgrandalcagaagatctcctgtacgccstcatgacctcccagggggtacccccactgagatatataggaagtacaacaagatggccgaggagcagtttgggggcaaccccctct  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA'  To R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCTGAGGGCATAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACCTTCCTGGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960 I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCCCTTTTTCCCTTATTTTCCCTAGGGTGTTTTTTGGCTTGGGTTTTTTTGGGTTGGTT   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRG*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCAGTTGTTCCTTCTTCTTT  TQRRLSQLLRELELYGLVEILVAGGGCCTAGGGGCCTTGTCAGGATTTTTGCCTGGGGGCACTTTTTTGCCTGTAGTTTTTTTT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC   
  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRG*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCAGTTGTTCCTTCTTCTTT  TQRRLSQLLRELELYGLVEILVAGGGCCTAGGGGCCTTGTCAGGATTTTTGCCTGGGGGCACTTTTTTGCCTGTAGTTTTTTTT  | Transparacy Comparison of the  | Transpagacian Comparation of the state of th | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACCTCATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  
       | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACCTCATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RL P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RCCCAGAGGGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTGCGCAGGGGCCTGGGGAGGGGGGTTACTGGCATGTTGTTCTTCTCTTT  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  B1 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTAATTTTTTACCTAAGGGTGTTTTT  1 D P D L N L E A 1 R R S L *  B61 TAGGTGGCTAAGCAGAATTCTGAAGGGCTGGCCACCGCCATTTTTCCCTTAAGGGTGTTATTTTACATACTTATAACTTATAACTGTATACATAC  |
| 601 TTGAGGGACAACCAGAAGATCCTCCTGTAGGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCACCTTTTGGGGGCACCCCCCL L R D N Q K I L L Y A V M T S Q G G T P T E T Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M QRF8'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGCGCGAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTTCTCTT  | CSTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC V M T S Q G G T P T E Y Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M CMF8' ACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTTGTCTCTCTC   | Transparacy of the properties  | COLUMN TO A CAGAGAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACGCCCTC  LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTTETYRKYNKMAEEQFGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGACCTTCCCAGCTCCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGTTGTGGGGGGGG   | Transgrandaraccaragaractcctctgacccccactgacctccccactgaccatatatat  | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   
                 | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   | Transgraftalagaagattttagagattttagagattttagagatttagagattatattagaaga   | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   | Tragggacaaccagaagatcctcctgtacgccgtcatgacctcccagggggatacccccactgagatatataggaagtacaacaagatgccgaggacatttggggcacacccctctctct   |
Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctccccccactgagatatatat   | Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctccccccactgagatatatat   |
Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | Transgraftalagaarattitagaarattitagaarattitagaarattitagaarataaragaarattitagaa | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGACGTTTGGGGGGCAACCCCTC  LRONQKILLYAVNTSQGGTPTETYRKYNKMAAEEQFGGNAACCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRHOMER*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTTGACGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCAACTTGCTGAGGTTGTCCGCAGGGGCCAGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   
   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCCC  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGGGAGAGGAGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVNTSQGGTPTEIYRKYNKHALEQFGGGAGGGGGAGTTTGGGGGCAACCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKHALEQFGGGGAGGGGGGAGTTTCTCTCTCTCT  ACGCAGAGGAGGAGTTCCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGGAGGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGACGTTTGGGGGGCAACCCCTC  LRONQKILLYAVNTSQGGTPTETYRKYNKMAAEEQFGGNAACCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRHOMER*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGCAACTTGACGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCAACTTGCTGAGGTTGTCCGCAGGGGCCAGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACAACAAGATGGCGGGGAGAGGAGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVNTSQGGTPTEIYRKYNKHALEQFGGGAGGGGGAGTTTGGGGGCAACCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKHALEQFGGGGAGGGGGGAGTTTCTCTCTCTCT  ACGCAGAGGAGGAGTTCCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGGAGGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTCTCTC   
   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCCCC  | Transgraftaraccagaagatctcctgtacgccgtcatgacctcccagggggstaccccactgagatatataggaagtacaacaagatgccgagggagcatttggggcaacacccctctccccccactgagatatatat  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT   | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT   
  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFG6NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGE6'  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCAGATTGAGGTTGCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCTCCTCTT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCAGAATTGAGGTTGCGCGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTCTCCTCTT  TQRRLSQLLRELELYGLVEIVGRACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATAGACCTCATAGTTTTT  P60  ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTTATGACCTCATAGTTTTT  AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACAGGGTTGTTT  AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGTTATATAACTTATATAAGGATGACTGTCAGAGTACCTTAAA  1080  AGGGGTGTTTTGATGAGAATTTAGAGGCCTACCAAAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGGTTGGTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGAGCAGTTTGGGGGCAACCCCTCTCTCT   | Transpagacian Correspondence Contragacio Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Conservati | Transpagacian Correspondence Contragacio Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Concerca Conservation Conservati | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT   
  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRONQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFFGENACCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  721 ACGCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGGTGGGAGGGGGGGTTACCTGCACTCTCTCT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCCATTTGGGGGCAACCCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RL P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCTCTTT  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTGAGGTTGTCGGCAGGGGCCGTGGGGAGGGGGGTTAACTGGCATTGTTCTTCTCTCTTTTTAGACCTCATAGTTTTT  B40  ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  AGGGGTGTTTTTGATGGAATTCTGAAGGGCTGCCACCGCCATTTTCGCTTGATTTTGCCAGAGCCATTTTTGCGTTGGTTTTTTTGGGTGGG  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCATTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKMAEEQFGGAGCATTTGGGGGCAACCCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAACCTCATGGCCTTGTGGGGAACTTGAGGTTGTCGGGGGGGG  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFG6NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRB*  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGCGCGAGGGGCCGTGGGAGGGGGGTTAACTGGCCTTGTCCTCTCTCT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGAACTTTGGGGGCAACCCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGAACTTTGGGCTTGCTCTCTCTCT RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGGGCTTGCTCTCTCTCTCT ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCGGGGGGGG   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGAGCAGTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTEIYRKYNKMAEEQFGGAACTTTGGGGGCAACCCCCTC RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGAGGGAGCTTGGGGAGGAGCTTCTCTCTCTCT  RLPPKGLEQPFKFEIAKDLNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  | Tragaggacaaccagaagatcctcctgtacgccgtcatgaggggtacccccactgagatatataggaagtaccaaagatggccaaagataccccactgagatatataggagtaccaaagatggccaaagataccaaaataggccctc to be rong reference by reference refe | TIGAGGGACAACCAGAAGATCCTCGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGGTPTEEYRKYNKMAEEQFGGGTACCCCACTGAGATATATAGGAAGTACAAAAAGAGGTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEYYRKYNKMAEEQFGGAACTGTGGGCAGGGCACTTCTCCTCT  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTCCTCTCTT  TQRRLSQLLRELFLYGLVFGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGGTGAACTCCCTATTTTTTAGACCTCATAGTTTTT  P60  1 OPDLNLEAIR RSL*  1080  AGGGGTGTTTTCATGGAACTCTGAAGGGCTGCCCACCGCCATTTTTCCCTTATTTTCCTAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  AGGGGTGTTTTCATGGAATTTAGACGCCATTTTACTACAAAAAACTGTTGTATATTTTCCAGGCCAGTTCTATTTTTTGGTGGCTGCTGACGGCCATGCCAAACACATCCTAAA  1200  BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGGAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCCTGAATGATGACGATGCCCTAACTGCCCTATCTGCT  1320  BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGCAACTTTTTCGACGGGAATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320 
BAAATTGATGAGAATTTAAGGCAAACTATTAGGGCGCAACTTTTTCGACGGGAATTTACCAAAGAAGTTTTTGAGGACCCTTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320   | TIGAGGGACACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACACAAGATGGCGAGAGAGA   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTYPTEIYRKYNKMAEEQFGGAGCTTTGGGGGCAACCCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTEIYRKYNKMAEEQFGGGGGGGTACCTCTCTCTCTT  ACGCAGAGGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGCTGCAGGTTGTCGGCGGGGGGGG  | Transparacionacionacionacionacionacionacionacion  | Transparacionacionacionacionacionacionacionacion  | Transgrandalcagaagatctcctgtacgccstcatgacctcccagggggtacccccactgagatatataggaagtacaacaagatggccgaggagcagtttgggggcaaccccctct  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA'  To R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCTGAGGGCATAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACCTTCCTGGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960 I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCCCTTTTTCCCTTATTTTCCCTAGGGTGTTTTTTGGCTTGGGTTTTTTTGGGTTGGTT   | Transgrandalcagaagatctcctgtacgccstcatgacctcccagggggtacccccactgagatatataggaagtacaacaagatggccgaggagcagtttgggggcaaccccctct  L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA'  To R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCTGAGGGCATAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACCTTCCTGGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960 I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCCCTTTTTCCCTTATTTTCCCTAGGGTGTTTTTTGGCTTGGGTTTTTTTGGGTTGGTT   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRG*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCAGTTGTTCCTTCTTCTTT  TQRRLSQLLRELELYGLVEILVAGGGCCTTGCAGGAACTTGAACTCTATGGCCTTGTCAGGATTTTTTGCCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 DPDLNLEAIRRSCCTGAAGGAGCTGCACAGGGCCAACTTTTCCCTTGAGGCCAACTTCTCTGGATTTTTTGCCTGGATTTTTTGGGTGGACGCGAACTCCCTATTTTTTATGACCTCATAGTTTTT  961  1 TAGTTGGCCTAAGCAGATTCTGAAGGGCCTGCCCACCGCCATTTTTCGCTTGATTCCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTGATTACACTACTTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  961  1 TAGTTGGCTAAGCAGATTTTAGAGGCCTGCCACCGCCATTTTTCGCTTATTACACGATTCTTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  962  1 ORD  963  1 TAGTTGGCTAAGCAGAATTTAGAGGCCTGCCCACCGCCATTTTTCGCTTATTACACGCTTCGCCTATTTTGGGTTGGTT  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC   
  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC   | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACTCCCTCC  | TIGAGGGACAACCAGAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGGCAACGCCCTC LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGGAACTTTGGGGGCAACGCCCTC  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRG*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCAGTTGTTCCTTCTTCTTT  TQRRLSQLLRELELYGLVEILVAGGGCCTTGCAGGAACTTGAACTCTATGGCCTTGTCAGGATTTTTTGCCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 DPDLNLEAIRRSCCTGAAGGAGCTGCACAGGGCCAACTTTTCCCTTGAGGCCAACTTCTCTGGATTTTTTGCCTGGATTTTTTGGGTGGACGCGAACTCCCTATTTTTTATGACCTCATAGTTTTT  961  1 TAGTTGGCCTAAGCAGATTCTGAAGGGCCTGCCCACCGCCATTTTTCGCTTGATTCCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTGATTACACTACTTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  961  1 TAGTTGGCTAAGCAGATTTTAGAGGCCTGCCACCGCCATTTTTCGCTTATTACACGATTCTTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1 ORD  962  1 ORD  963  1 TAGTTGGCTAAGCAGAATTTAGAGGCCTGCCCACCGCCATTTTTCGCTTATTACACGCTTCGCCTATTTTGGGTTGGTT  | Transparacy Comparison of the  | Transpagacian Comparation of the state of th | TIGAGGGACAACCASAAGATCCTCCTGTACGCCGTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGGGCAACTTTGGGGGCAACCCCCTC LRDNQKILLYAVMTSQGGTTPTETYRKYNKMAEEQFGGAGCAGTTTGGGGGCAACCCCTCTC  RLPPKGLEQPFKFEIAKDLNLNDAPTETYRKYNKMAEEQFGGGAGGGGGCAACTTTCTCTCTCT  ACGCAGAGGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATAGGCTTGCAGAGTTGGGGCTGGGAGGGGGGGTTAACTGGCATTGTCCTTCTTCTTCTT  TQRRLSQLLRELELYGLYGLYEIEVVGRGRRGCCGTGGGAGGGGGGTTAACCTGAGGTTTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT   
  | TIGAGGGACAACCAGAAGATCTCCTGTACGCCGCCATCTCCAGGGGGGTACCCCCCACTGAGATATATAGGAAGTACACCAGATGACGAGATGTTTGGGGGGCAACCCCTC  LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAAEEQFFG8NAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGF8'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGCAACTGAACTCTATGGCCTTGTGGAGATTGAGGGTTGTCGGCAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT  TQRRLSQLLRELELYGLYELYGLYELYGAGGCCATTTTTCTCTGAGGTTGTTCGGGAGGGGGCGGTGGGAGGGGGGTTAACTGGCATGTTTTTTTT  | TIGAGGGACAACCASAAGATCCTCCTGTACGCCSTCATGACCTCCCAGGGGGGTACCCCCACTGAGATATATAGGAAGTACAACAAGATGGCCGAGGAGCAGTTTGGGGGCAACGCCCTC  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RL P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  RCCCAGAGGGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTGCGCAGGGGCCTGGGGAGGGGGGTTACTGGCATGTTGTTCTTCTCTTT  T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  B1 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTAATTTTTTACCTAAGGGTGTTTTT  1 D P D L N L E A 1 R R S L *  B61 TAGGTGGCTAAGCAGAATTCTGAAGGGCTGGCCACCGCCATTTTTCCCTTAAGGGTGTTATTTTACATACTTATAACTTATAACTGTATACATAC  |
| L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACCCAGAGGAGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGATGTTTTTTGCCTAGTGTTTTTTTT  | W M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  K F E I A K D L N L N D A P A T P P P N V R M ORF8'  ACTTGAACTCTATGGCTTGTGGACATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGCATGTTGTCCTTCTCTCT  L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D .  GAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  R S L *  CACCGCCATTTTTGCCTGCATTCTATATAACTTATAACTTATAAGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  TACTACAAAAGAGTGGTTGATATTACAGGCTACTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGCCTTGTCGAGATTGAGGTGTGCGCAGGGGCGTGGGAGGGGGGTTAACTGCCAGTTGTTCCTTCT T T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGGTAAGCAGAATTTGAGGGCTGCCACCCCCATTTTTCCCTTATTTACCTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGCATTCTATTAACTTATTAGGTGGTGTTTTTTGGTGGTGCTGCTGACGGCCATGCCAAAA  1201 GAAATTGATGAGAATTTAAGGCAGAACTATTAGGGGGCAACTTTTTCGAGGATTTTTCGAGGATTTTTTGGGTTGGTT   | LRDNQKILLYAVMISQGGGTPTELYRKYNKMAREQFGGAACTTCAAAGAGGTCTTCTCTTCTCTT  RLPPKGLEQPFKFEIAKDLTAACTTCAAGAGGGGGCCTTGGGGAACTTGAACTTCTTCTCTCTT  ACCCAGAGGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGCAGGGGGCCGTGGGAGGGGGGGTTAACTGGCTGTTGTTCCTTCTTCTTCTTT  TQRRLSQLLRELELYGLYGLYGGAGGACTTTCCCAGGGAACTTGAGCTTGTCGCAGGGGGCAACTTTTTCCTGGATTTTTGCCTGTAGGAGTAACTCCCTATTTTTTAAGGCTCATAGTTTTT  P60  1 TAGTTGGCCTGACCTCATGCTTGAGGGCAACTGTTTTCGCTTAACTTAAGGGGGAACTTTTTGCCTGTAAGTAA  | LRONQKILLYAVMISQGGGTPTEEIYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLN LNLNDAPATPPPNVRMGRS  721 ACCCAGAGGAGGGCTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGTCGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCTGTTGTTCCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGRCCATGTGTTTTCTCCTCT TQRRLSQLLRELELYGLVEIEVVGRRGRCCATGTGTGTCGCAGGGGCGGGGGGGGGGGGGGGG  |
LRONQKILLYAVMISQGGGTPTEIYRKYNKMAREQFGGGAACTTAAAGAGGAACTTAAAGAGGAACTTAAACTTATAACTTATAAGGAGGAACTTAAAGAGTGTTTTT  721 ACGCAGAGGAGGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTTCTCTCTC   | LRONQKILLYAVMISQGGGTPTEIYRKYNKMAREQFGGGAACTTAAAGAGGAACTTAAAGAGGAACTTAAACTTATAACTTATAAGGAGGAACTTAAAGAGTGTTTTT  721 ACGCAGAGGAGGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTTCTCTCTC   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | LRONQKILLYAVMISQGGGTPTEIYRKYNKMAREQFGGGAACTTAAAGAGGAACTTAAAGAGGAACTTAAACTTATAACTTATAAGGAGGAACTTAAAGAGTGTTTTT  721 ACGCAGAGGAGGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTTCTCTCTC   | LRONQKILLYAVMISQGGGTPTEIYRKYNKMAREQFGGGAACTTAAAGAGGAACTTAAAGAGGAACTTAAACTTATAACTTATAAGGAGGAACTTAAAGAGTGTTTTT  721 ACGCAGAGGAGGGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTTCTCTCTC   
   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | LRDNQKILLYAVMTSQGGGTPTEEYYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGGAACTTGACTCTATGGCCTTGTCGAGATTGAGGTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGCCTGTTGTTCCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGTGGGAGGGGGGGAACTTGTCTCTCTCTTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | LRDNQKILLYAVMTSQGGGTPTEEYYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGGAACTTGACTCTATGGCCTTGTCGAGATTGAGGTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGCCTGTTGTTCCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGTGGGAGGGGGGGAACTTGTCTCTCTCTTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT  
  | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | LRDNQKILLYAVMISQGGGTPTEEIYRKYNKMAREQFGGGAACTTCAACTCATCTTTTTTTTTTTTTTTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  
   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTTGCTTGATGGATG   
  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA.  721 ACCCAGAGGAGGACCTTTCCCACTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGTCTTCTTCTTTTTT  1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGAGAACTTTAGAGGCCTGCCCACCCCCATTTTTCGCTTGATATTACAGGATGATTATATAAGGATGACTGTTACAGTATCTTTACAGGGTGTTTTT  1 Q P D L N L E A I R R S L **  963 AGGGGTGTTTTGATGGAATTTAGAGGCTGCCACCCCCATTTTTCGCTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTTTTTGGTTGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA.  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGACTTGACTCTATGGCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCASCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCAACTTGAACGTCCTGAGGGCAACCTTGCCAGGGGCAACTTTCTCTGGATTTTTGCCTGGATTTTTTATGACCTCATGGTTTTTT 960  961 TTAGTTGGCTAGAGAGACTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTGATTTCCTGGATTTTTTGCTTGATGGATG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR.  721 ACGCAGAGGAGGTTTCCCACCTCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCCATTTTTTATAGACTCCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATATTTTCCCTGGATTTTTGGCTGGATGTTTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA.  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGACTTGACTCTATGGCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTTTTTT  
  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFA.  721 ACCCAGAGGAGGACCTTTCCCACTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCCGCAGGGGCCGTGGGAGGGGGGGTTTACCTGTCTTCTTCTTTTTT  1 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGAGAACTTTAGAGGCCTGCCCACCCCCATTTTTCGCTTGATATTACAGGATGATTATATAAGGATGACTGTTACAGTATCTTTACAGGGTGTTTTT  1 Q P D L N L E A I R R S L **  963 AGGGGTGTTTTGATGGAATTTAGAGGCTGCCACCCCCATTTTTCGCTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTTTTTGGTTGG  | LRDNQKILLYAVMTSQGGGTPTEEYYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGGAACTTGACTCTATGGCCTTGTCGAGATTGAGGTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGCCTGTTGTTCCTCTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGTGGGAGGGGGGGAACTTGTCTCTCTCTTT TQRRLSQLLRELELYGLVEIEVVGRRGCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT   | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  
   | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFFGGNALTCTTTAGGGTTGTCTCTTCTCTTT  RLPPKGLEQPFKFEIAKDLNINGGGGGGCTTTGCAGGGACTTGAACTCTATGGCTTGTCGAGTTGTGGCAGGGGGGGG   | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFFGGNALTCTTTAGGGTTGTCTCTTCTCTTT  RLPPKGLEQPFKFEIAKDLNINGGGGGGCTTTGCAGGGACTTGAACTCTATGGCTTGTCGAGTTGTGGCAGGGGGGGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCTTGTGGACTTGTGGCAGGGGGCGGGGGGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGACTTGACCTCTATGCCTTGCGACATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGCGTTACTGCTGTTTTCTCCTCT I Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 0 P D L N L E A J R R S L -  961 TTAGTTGGCTAGCAGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATTTCCAGAGGCTAACTTTAGAGTATTTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGACCTTTCCCACCCCCTGAGGGACCTGACCCTGAGGCCTTGCGACATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGCGTTACCTGCTGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATAGACCCCTATTTTTTATAGACCCCTATTTTTTAGACCCCCATTTTTCGTTGTTCTTCTTCTTCTTCTTTTTTTT  
  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGACCTTTCCCACCCCCTGAGGGACCTGACCCTGAGGCCTTGCGACATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGCGTTACCTGCTGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATAGACCCCTATTTTTTATAGACCCCTATTTTTTAGACCCCCATTTTTCGTTGTTCTTCTTCTTCTTCTTTTTTTT   | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFFGGNALTCHTAGGCTTGTCAGATTGAGGTGTCGGGGGGGGGGGGGG   | LRDNQKILLYAAVMITSQGGGTTPTETYRKYNKMAEEQFFGGNALTTAAGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTGTCGCCAGGGGGCCGTGGGAGGGGGGTTACCTGCTCTTCTCCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCCAACTTTCTCTGGATTTTTGCCTGAATTTTTGCCTGAATTTTTATATAGGATGACTGCTAAGTATTTTTAGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGCAGAATTCTGAAGGGCTGCCCCCCCATTTTTCCCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCAGGGTGTTTTT  AGGGGTGTTTTGATGGAATTTAGAGGCCATCTAAAAAGAGTGGTTGATATTACAGCGTTTTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACCCAGAGGAGGCTTTCCCACCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGCTCTTCTCCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGGTATCTTTACAGGGTGTTGTT  1 0 P D L N L E A I R R S L **  962  963 TA P T E I Y R K Y N K M A E E Q F G G N A L  864  865  866  866  867  868  869  869  869  860  860  860  860   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721
ACGCAGAGGAGCTTTCCCAGCTCCTGAGGAACTTGACCTCTATGGCCTTGTCGAGTTGTGCGCAGGGGGCGGGGGGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR.  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGACTTGAGGTGTCGGCAGGGGGCGGGGGGGG  | L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K H A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGGGCTTTCCCAGCTCCTGAGGGAACTTGACTCTATGGCCTTGTCGAGATTGAGGTTGTTCGCCAGGGGGCGTGGGAGGGGGGTTACTGCATGTTTTCTCTCTC  | LRDNQKILLYAVMTSQGGGTTTTECTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT   | L R D N Q K I L L Y A V M T S Q G G T P T E I Y R K Y N K M A E E Q F G G N A L  R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8'  721 ACGCAGAGGAGCTTTCCCACCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCGTGGGAGGGGGGTTAACTGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W M V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 0 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCTCCTTATTTGCCAGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGATATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGATTTTAGAGGCCATTTTACTACAAAAGAGTTGTTATATAACTTATAACTTATATAGGATGACTGCTGCTGACGGCCATGCCTAAGTTCTTAACTGAACTGCTAAGGATGCTGACGGCCATGCCTAAGGATCCTAAA  1200 GRF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGAACTTTTTCCACGGGGATTCCCAAAGAAGTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGTTAACTGGCATGTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCGGATTTTTGCCTGAGTGTTTTTTTAGCCTCATGTTTTTT 960  1 0 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTCCGCTTATTTGCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081
AGGGGTGTTTTGATGGAATTCTGAAGGGCCTGCCACCGCCATTTTCCGCTTGATTTTCCCAGAGCCTGCTTGGTTTTTTTGGTTGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTAGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGATTTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATATACAGCTTCGCTTATTTGGTTGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS.  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTAGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGATTTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATATACAGCTTCGCTTATTTGGTTGG   | LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACCCAGAGGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTGTTCCTCTCTTCTTT TQRRLSQLLRELELYGLVEIEVVGRRGRACTTGAGCCTATGGCCTTGTGCCTGAGGCTGTGTGTGCGCAGGGGGCGTGGGAGGGGGGGTTAACTGGCATGTTTTCTCTCTC   | LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACCCAGAGGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTGTTCCTCTCTTCTTT TQRRLSQLLRELELYGLVEIEVVGRRGRACTTGAGCCTATGGCCTTGTGCCTGAGGCTGTGTGTGCGCAGGGGGCGTGGGAGGGGGGGTTAACTGGCATGTTTTCTCTCTC   | LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGR8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGTCGAGATTGAGGTGTCGCGCAGGGGGCGTGGGAGGGGGGTTAACTGCCATGTTTGTCCTTCTCTTT TQRRLSQLLRELELYGLVEIEVVGRGGCCGTGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGTTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATGGGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACTTTTTCGCTTGATATATAT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGTTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATGGGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACTTTTTCGCTTGATATATAT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGTTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAAGGCTGCCACTTTTTCGCTTGATTATTAACTTAATAGGTGAACTGCTTAACTTAAGGATTCTTTAACTAAGGTGTTTTTTTT   
   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGTTGTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTGTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATGGGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCACTTTTTCGCTTGATATATAT  | LRDNQKILLYAVMTSQGGTPTETYRKYNKMAEEQFFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGR8*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGACCTCTATGGCCTTGTCGAGATTGAGGTGTCGCGCAGGGGGCGTGGGAGGGGGGTTAACTGCCATGTTTGTCCTTCTCTTT TQRRLSQLLRELELYGLVEIEVVGRGGCCGTGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGG  | LRDNQKILLYAVMTSQGGTPTEIYRKYNKMAEEQFGGNAL  RLPPKGLEQPFKFEIAKDLNLNDAPATPPPNVRMGRS*  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGCCATGTTTTCCTCTCT TQRRLSQLLRELELYGLVEIEVVGRRGRCGAGGGGCGTGGGAGGGGGGGGGGGGGGGGGGGGG   | LRONQKILLYAVMISQGGGTPTETETYRKYNKMAREQFGGNACTTAAGGGAACTTGAACTCTATGCCTTGTCGGAGTTGTGGGCGGGGGGGG   | LRDNQKILLYAVMTSQGGGTPTEETYRKYNKMAEEQFGGGCFGGGACTTAAAGGGACTTGAACTAAGGATTTTTAAGGAGGGGCTTTCCAGAGGAGAGAGGACTTTCCTCTCTCT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR.  721 ACGCAGAGGAGGTTTCCCACCTCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCCATTTTTTATAGACTCCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATATTTTCCCTGGATTTTTGGCTGGATGTTTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR.  721
ACGCAGAGGAGGTTTCCCACCTCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCCATTTTTTATAGACTCCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATATTTTCCCTGGATTTTTGGCTGGATGTTTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR.  721 ACGCAGAGGAGGTTTCCCACCTCTGAGGGACTTGACCTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGGTTTACCTGTGTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCCATTTTTTATAGACTCCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTGATATTTTCCCTGGATTTTTGGCTGGATGTTTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N GRB'  721 ACGCAGAGGAGCTITOCCACCTCCTGAGGGAACTIGACTCTATGGCCTTGTCGACATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCC  |
| R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N Y R N ORF8'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W N V V P S S  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTT I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTG 1081 AGGGCTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGGTTGTTGATTTACAGCCCTTATTTTGGTTGG   | K F E I A K D L N L N D A P A T P P P N V R M ORFR'  ACTIGAACTCTATGCCTYGTCGAGATTGAGGTTGTCGGCAGGGGGCGGGGGGGGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTGAGTGTAACTTATTATGACCTCATTTTTTTATGACCTCATAGTTTTT 960 I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGAGAATTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATTAACTTATATAGGTGACCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGAGGAATTTGAGGACCCCATTTTACTAAAGAGGTGTTGATATTAACTTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTYGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTATGACCTCATAGTTTTT 1 D P D L N L E A 1 R R S L °  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTGATGGAATTTAGAGGCCGCATTTTACACAAAAGAGTGGTTGATATTACAGGCTGCTGGTTTTTTTGGTGGCTGCTGAGGGCCATGCAGATCCTAAA 0 ORF11 M E F R R H F T T K E W L 1 L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCCAAGATCCTAAATTAGGATGAGAAATTTAAGGCATGACGATGCCTATTTGGTTGCT 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTTCTTTTGGGGGAAGATACCAGAGCCGAAAATTTCAAAGATTACGTAATATGGCTTTTAAAATT 1440  V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTGTGGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAACTTGAGGGCTGCCACCCCCATTTTTCCCTTATTTTCCCTTATTAACTTATATAGGTGACCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACAAAAGAGTGGTTGATATTACAGCTTCCCTATTTTGGGTTGGGTTTTTTGGGTGGG  | R L P P K G
L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGTGAGTCTCTAGTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGTGAGTCTCTAGTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTACTTAGAGTACCTCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATAT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGGAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGCCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGGAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGCCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   
   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTACTTAGAGTACCTCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATAT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTGCCTGAGGCCAACTTCTATTAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 1081 AGGGGTGTTTTGAGGAACTTTAGAGGCCCCCCATTTTTCGCTAATTACAGGCTTCCCCTATTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTACTTAGAGTACCTCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATAT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT   
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   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCACCCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTTAGAGGCCACCCCCATTTTCCGCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAGAGGCCACCCCCATTTTTCGATATATACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGACCTCTATGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  10 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGCCAGTTCTATATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCCATTTTACTACAAAAGAGTGGTTGATTTTCCCAGGCCAGTTCTATATAACTTATATGGGTGGTTTTTTTT  
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GAAATTGATGGAAACTTTAGGCAGAACTATTAGGGCGACACTTTTTCGCGGGAAGTTTACCAAGAAGTTTTTAGGGGCAACTTTAGAGGATGACGATGACGATGCCCTATCTGCT  1320  1321 GTAGTAGAAACTTTAGACCCCCTTAGAGGGATTAAAGGCGGTTCATTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGACCTCTATGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  10 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATTATCAAGCTTCTATATAACTTATATAGGATGACGTTCTCTGACGGCCATCCAGATTCTAAA  1200 GAAATTGATGGAATTTAAGGCAGCAACTATTAGGGCGACACTTTTTCGCGGGATTTTACAGAGATTTTTTAGGGCGCCATCCCAGATCCTAAC  1201 GAAATTGATGGAAACTTTAGGCAGAACTATTAGGGCGACACTTTTTCGCGGGAAGTTTACCAAGAAGTTTTTAGGGGCAACTTTAGAGGATGACGATGACGATGCCCTATCTGCT  1320  1321 GTAGTAGAAACTTTAGACCCCCTTAGAGGGATTAAAGGCGGTTCATTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGGTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGCTTTGAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACAAAAAGAGTGGTTGATATTACAGCCTTCTATATAACTTATATAGGATGACGTTCTCTACAGGTGTTGTT 1200  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAGGGCAGACTATTAGGGCGCAACTTTTTCGACGGGATTTACCAAGAAGTTTTTAGGGTGACCCTGAATGACGATGCCCTATCTGCT 1320  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1320 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCATTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCGAGTTGAGGTTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGCTTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCCATATTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGACCTCTATGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  10 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATTATCAAGCTTCTATATAACTTATATAGGATGACGTTCTCTGACGGCCATCCAGATTCTAAA  1200 GAAATTGATGGAATTTAAGGCAGCAACTATTAGGGCGACACTTTTTCGCGGGATTTTACAGAGATTTTTTAGGGCGCCATCCCAGATCCTAAC  1201 GAAATTGATGGAAACTTTAGGCAGAACTATTAGGGCGACACTTTTTCGCGGGAAGTTTACCAAGAAGTTTTTAGGGGCAACTTTAGAGGATGACGATGACGATGCCCTATCTGCT  1320  1321 GTAGTAGAAACTTTAGACCCCCTTAGAGGGATTAAAGGCGGTTCATTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961
TTAGTTGGCTAGACAGAATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATTATTACAGCTTCTATATAACTTATATAGGATGACGTTCCTCAGGGCCATCCAGATCCTAAA  1200 BAAATTGATGAGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGATTTTTTAGGGTGGTTTTTTGGGTTGGGTTTTTTGGGTTGGGTTGGGTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCGAGTTGAGGTTGCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGCTTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCCATATTTTGGGTTGGTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGGTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGCTTTGAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACAAAAAGAGTGGTTGATATTACAGCCTTCTATATAACTTATATAGGATGACGTTCTCTACAGGTGTTGTT 1200  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAGGGCAGACTATTAGGGCGCAACTTTTTCGACGGGATTTACCAAGAAGTTTTTAGGGTGACCCTGAATGACGATGCCCTATCTGCT 1320  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1320 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCATTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGAACTCCCTATTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTGCCTGAGGCCAACTTCTATTAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 1081 AGGGGTGTTTTGAGGAACTTTAGAGGCCCCCCATTTTTCGCTAATTACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961
TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCTTGTCGAGATTGAGGTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCTTCTTCTTCTT  7 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTCCCTTATTTGCCTGAGTTCTTATAACTTATATAGGTGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGCTGCTGCTGACGGCCATGCAGATCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAAGGCCCATTTTACTACAAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCTTGTCGAGATTGAGGTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCTTCTTCTTCTT  7 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTCCCTTATTTGCCTGAGTTCTTATAACTTATATAGGTGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGCTGCTGCTGACGGCCATGCAGATCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAAGGCCCATTTTACTACAAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCTGCCACCCCCATTTTTCGCTTGATTACTCATATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  AGGGGTGTTTTGATGGAATTTTAGACGCCATTTTACAAAAAGGTGGTTGATATTACAGGCTTCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCCTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCACAATTCTGAGGGCTGCCCACCCCCATTTTTCGCTTATTTACCTAATTAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTTAGAGGCCTGCCCACCCCCATTTTTCGCTTATTTACTTAATTAA  
   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCTGCCCACCCCCATTTTTCGCTTATTTACCTAATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGGTTTTTTGGGTGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGAACTTGAACTCTATGGCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCTGCCCACCCCCATTTTTCGCTTATTTACCTAATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGGTTTTTTGGGTGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCTTGTCGAGATTGAGGTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCCTTCTTCTTCTTCTT  7 Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTCCCTTATTTGCCTGAGTTCTTATAACTTATATAGGTGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGCTGCTGCTGACGGCCATGCAGATCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAAGGCCCATTTTACTACAAAAAGAGTGGTTGATATTAACTAATTAACTTATATGGGTGGG  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGACTCTCCAGCTCCTGAGGAACTGAACTCATGGCCTGTGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGTTAACTGCCATGTTTCTCCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTAGACCTCATAGTTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAGGGCTGCCACCGCCATTTTTCCCTTGAGGCTAACTTGCCTGATTTTTTGCCTGAGTGTTTTTAGAGTGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTGATGAGAATTTAGAGGCCCACCGCCATTTTCCCTTATTTTGCCAGGGCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721
ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTACCTAAGGATGTTTTTT 960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATATACAGGCTGCTCGTTTTTTTGGGTGGCTGCTGAGGGCCATGCCAGATCCTAAA QRF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCCAGACTATTAGGGGGGCAACTTTTTCGACGGGGATTTACCAAAGAGAGTTTTTGAGGACCATGCAAGATCCTAAA T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTTGGGGGAAGAATTTCAAAGAACATTACGTAATATGGCTTTTAAAATT 1440  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTACCTAAGGGTGTTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTTAGAGGCCATTTTACAAAAAGGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTGGCTTGCTGAGGGCCATGCCAGATCCTAAA  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCCAGACTATTAGGGGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGAACCATGCTACATGCACCTGAATGACGACGTCCCTATTTGGCT  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTTCTTTTTGGGGGAAGATTCCAAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT  1440  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCTTGTCGAGATTGAGGTGTCGCGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTAGTAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTTCCCAGAGCAGTTCTAATAACTTATATAGGTGAACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTAGAGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGTTTATATACAGCATTCGCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGACTCCCAGCCCCTGAGGGACCTGAACCCTATGGCCTGCGGACTGCGCATGGGCCTGCGCGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTCTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTCTGAAGGGCTGCCACCGCCATTTTTCCCTTATTTTCCCAGCGCAGTTCTATTAACTTAATGGATGACTGTTAACAGTATCTTTAACTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTCTAAGGCCCACCCCCATTTTACTAAAAAGAGTGGTTGATAATTAACTAATTAGGATGACTGTTAACAGTATCTTTAACCTAAGGGTGTTGTT 1080  0RF11 M E F R R H F T T K E M L I L Q A S P I W Y G F L V A A A D G H A D P K  1201 GAAATTGAGGAATTTAAGGCAGACTATTAGGGGGGCAACTTTTTCGAGGGGAATTTACCAAAGAAGTTTTTAGGACCATGCACCTGAATGAGCATGCCCCTATCTGCT 1320  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTTTGGGGAGGAGAACTTTCAAAAGACCTTTCAAAAGTCCTTTTAAATT 1440  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORF8'  721 ACCCAGAGGAGCTTTCCCACCTCTAGGGAACTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCGTGGGAGGGGGTTAACTGCATGTTGTTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTGCCTGAGTGTTTTTTGCCTGAGTGTTTTTTTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  721 ACCCAGAGGAGGCTTTCCCAGCTCTAGGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGCCAGGGCGCGTGGGAGGGGGTTAACTGCACTTGTTCTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTCATCCTCTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L **  1081 AGGGGTGTTTTGATGGAATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGTGTTTTT  1080 AGGGGTGTTTTTGATGGAATTCTGAAGGCCACTTCTAACAAAAAGATGGTTGATATTACAGGCTTGCCTATTTTGGTGGCTGCTGCTGCTGCACCGCCAATCCTAAA  1200 AGAATTGATGAGAATTTAAGGCAACTATTAGGGCGGAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCCTGAATGACCACTGAATGACCAATGCCCTATTTGCTAAGGAATTTAAGGACGAATTCTAAA  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTTACCAAAGAAGTTTTTTGAGGACCATGCCTGAATGATGACGATGCCCTATCTGCT  1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORF8*  221 ACGCAGAGGAGGCTTTCCCACCTCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCGTGGAGGGGGGTTAACTGGCATGTTGTTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V
V G R G R G R G V N W H V V P S S S  Element D .  241 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGGTTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGCTGTTTTGATGGATTTTAGACGCCATTTTACTACAAAAGATGTGTATATTACGCCTTGGTTTTTTTGGTTGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTTATTTTGCCTGTAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTGCCTGAGTTTTTTACCTAAGGGTGTTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACCTCTAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTGCCTGAGTTTTTTACCTAAGGGTGTTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACCTCTAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTGCCTAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R N ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTGCCTAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCTATTTTGGGTTGGTT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTATATAACTTATATAGGTGACTGTTAAGATTACTTAACTTAACTTAAGTTATTTTTCCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCCCTTATTTCCCTAGGCCTATTTTATATAGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841
ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCCCTTATTTCCCTAGGCCTATTTTATATAGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTCTCT  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCCCTTATTTCCCTAGGCCTATTTTATATAGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGACTTGACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCTTCTTCTTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTATATAACTTATATAGGTGACTGTTAAGATTACTTAACTTAACTTAAGTTATTTTTCCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGTGAGTCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGAATCTGAAGGGCTGCCCACCTCCATTTTTCGCTTATTTGCCTAGTGGTTTTTTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0861 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACGCAGAGGAGGCTTTCCCACTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840 Element D +  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTACCTATGAGTTTTTTTT   
  | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFR'  721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGCCGTGGGAGGGGGGTTAACTGGCCTGTTTCTTCTTCTTCTTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGTTTTTTGCCTGAGTGTTTTTTAGGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTCCCTTATTTTCCCTAGAGTTTTTTTT   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAGACAGAATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCCATATTACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGACCTTCTGGTTTGGTTTGGTTTGGTTTGGTTGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAGACAGAATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCCATATTACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGACCTTCTGGTTTGGTTTGGTTTGGTTTGGTTGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R M ORFS  721 ACGCAGAGGAGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCTTGCAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  840  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A I R R S L *  961 TTAGTTGGCTAGACAGAATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCCATATTACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTI  1080  1081 AGGGGTGTTTTGATGGAATTTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGACCTTCTGGTTTGGTTTGGTTTGGTTTGGTTGG   | R L P P K G L E Q P F K F E I A K D L N L N D A P A T P P P N V R H ORF8'  ACGCAGAGGAGCTTTOCCAGCTCTGAGGAACTTGACCTCTAGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCGTGGGAGGGGGGTAACTGCACTGTGTTCCTCTCTCT   |
| 721 ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGGGGGGGG  | ACTIGAACTCTATGGCCTYGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGCCATGTTGTTCCTTCTTCTCTT  L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  GAGGTCCCCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  R S L *  CACCGCCATTTTTGCCTTATTTGCCAGGGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  TACTACAAAAGAGTGGTTGATATTACAGGCTTGCCCTATTTTGGGTTGGTT  | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGAGATTGAGGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGAGAACTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTGGGTTGGATTTTTGCTAAGGATTCTTAACAGAGTGTTGTTT  1080  961 AGGGGTGTTTTGATGGAATTTAGAGGCCTGCCACCGCCACTTTTTCGCTTATTTACAGAGTTTTTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGAGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTTTTGCCTGTAAGTACTTTAACTGAGTACTCTTAAGGATGACTGTTCAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTTACTACAAAAGAGTGGTTGATTTTACAGGCTTCGCTTATTTGGGTTGGTT   | 721
ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTTTGCCTGTAGAGTACCTGTAACAGTAGTTCTTTAACTAAC  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTTTGCCTGTAGAGTACCTGTAACAGTAGTTCTTTAACTAAC  | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTTTGCCTGTAGAGTACCTGTAACAGTAGTTCTTTAACTAAC  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTTTGCCTGTAGAGTACCTGTAACAGTAGTTCTTTAACTAAC  
   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATTTTTCTCTCTC  | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT  
  | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGAGTTCTTTAACTAGGATGCTTTAACAGAAGAGTGGTTGTT  1080  1081 AGGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATTTTTCTCTCTC  
   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTITCCCAGCTCCTGAGGGAACTIGAACTICATGGCCTTGTCAGAGTTGTCGGCAGGGGGCGTTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTTGAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTGGATTGTTTAGAGTGACTGTTACAGGATTCTTAACGGTTGTTTT  1080 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCACCCCCACCTTTTTCGCTTATTTCCCAGGGGCAACTTTTTGGGTTGGTT   | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   
  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  
   | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACCTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCAGAGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCACCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAAATTTAAGGCCACCCCCATTTTTCCACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGAGGTTGTCGGCAGGGGGGCGTTGAGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTT T Q R R L S Q L L R E L E L Y G L Y E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGTACTTCCCATAGTTTTTTTT   
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1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCGCCATTTTTCGCTTATTTCGCAGGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  961 ITAGTTGGCTAAGCAGATTTAGAGGCCGCCACCCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTCTAGAGGCCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTTAGAGCCCATTTTACCAAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGTTGG   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTCTAGAGGCCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTTAGAGCCCATTTTACCAAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGTTGG   | Page 1 of the property of the  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTTAGAGGCCATCTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT  | 721 ACCCAGAGGAGGACCTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTAATAAGGTGACTGCTAAGAGTACTTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCCCCATTTTTACTACAAAAGAGTGGTTGGT  
  | 721 ACCCAGAGGAGGACCTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTAATAAGGTGACTGCTAAGAGTACTTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCCCCATTTTTACTACAAAAGAGTGGTTGGT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  961 ITAGTTGGCTAAGCAGATTTAGAGGCCGCCACCCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  961 ITAGTTGGCTAAGCAGATTTAGAGGCCGCCACCCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTCTAGAGGCCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGCTGTTTTGATGGAATTTAGAGCCCATTTTACCAAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGTTGG   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCTCTCTC   | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGTAGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCCACTTTTTCGCTTATTTTGCCAGCGCAACTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTTGGGTTGGGTTTTTTGGGTTGGGTTTTTTGGGTTGGGTTTT  | ACCCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGAA  
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961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGCGCAGTTCTATAACACTTATATAGGTAGAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGAGAATTTGAAGGGCTGCCCACCCCCATTTTCCCTTATTTCCCTAAGGGTCTCTATATAACTTATATAGGTGAGTGA   | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGAGAATTTGAAGGGCTGCCCACCCCCATTTTCCCTTATTTCCCTAAGGGTCTCTATATAACTTATATAGGTGAGTGA   | 721 ACCCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A J R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCTATACACTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RFI1 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K   | 721 ACCCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A J R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCTATACACTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RFI1 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K   | 721 ACGCÁGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCGCTTCTTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0751 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCTTCATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1080  0861 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCTTCATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1080  0861 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | 721 ACGCAGAGAGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961
TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTGCCTAATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCGCTTCATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTTGTTT  1080  0861 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | 721 ACGCÁGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCGCTTCTTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0751 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  | 721 ACGCAGAGAGAGCTTTCCCAGCTCCTGAGGAACTTGAACTCTATGGCCTTGTCAGATTGAGGTTGTCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A J R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCGCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0RF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K   | 721 ACCCAGAGGAGGACTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCAGAGTTGTGCGCAGGGGGCGTGGGAGGGGGGTTAACTGGCATGTTGTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGCTTCGCAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGCGGCAGTTCTATATAACTTAATAAGGTAGACTGCTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGACCTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTCCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  961 ITAGTTGGCTAAGCAGATTTAGAGGCCGCCACCCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGTACTTCCCATAGTTTTTTTT  
  | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGTACTTCCCATAGTTTTTTTT   | 721 ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGGCCGTGGGAGGGGGGTTAACTGGCATTTTTCTTCTCTT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G V N W H V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAATGTACTTCCCATAGTTTTTTTT   | ACGCAGAGGAGGCTTTCCCAGCTCCTGAGGGAACTTGAACTCTATGGCCTTGTCGAGATTGAGGTTGTCGGCAGGGGCCGTGGGAGGGGGGTTAACTGGCATTGTTCTTCTCTCT T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCCCTTATTTTGCCAGCGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTTT  |
| T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTT  I D P D L N L E A I R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTCGCTTATTTGCCTAGTTGCCTAATTAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTGGTTGG  | LELYGLVEIEWD CARGE REVVER REVVER REVVER REVVER REVVER REVVER RESULT TO THE RESULT OF T | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTCCCTTATTTCCCTAGGGCTAACTTCTATAACTTATAAGGTGGCTGCTGACGGCCATGCAAGATCCTAAA 1200  ORFI1 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGGGCAACTTTTTCGACGGGATTTTACCAAGAAGTTTTTGAGGACCATGCACCTGAATGACGATGCCCTATCTGCT 1320  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGAGCCCCTTAGAGGGGATTAAAGGGGGTTCTATTTTTGGGGAGAGCCCGAAAAATTTCAAAGAACCTTTAGAGAACCTTTAAAATT 1440   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W N W N V V P S S S  Flement D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGATAAGATTCTTAACGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCACCCCCATTTTTCCCATAGTTTTTCGCTTGGGTTTTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTCTATAACTTATATAGGATGACTGTTACAGATTCTTAACGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGAGATTTAGAGCCCATTTTACCAAAAGAGTGGTTGATATTACAGAGTTCTTATAACTTATATAGGATGACTGTTACAGTTTCTTACAGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGAGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGCTTCGGCTTTTTGGTTTGGTTTGGTTTTTTTGGTGGCTGCT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCTACGGGCAACTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAACTTAGAGCCCCATTTTACAAAAGAGTGGTTGATATTACAGCCTTCGCCTATTTTGGGTTGGGTTTTTTGGTTGG  
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   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCCTAGGGGCAACTTTCTCTGGATTTTTGGCTTGGTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCCTAGGGGCAACTTTCTCTGGATTTTTGGCTTGGTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCCTAGGGGCAACTTTCTCTGGATTTTTGGCTTGGTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTTGAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCTAGGGCTATTTTGGCTTGGTTTGGTTGG  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTAGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCCATTTTTCGCTTATTTCCCTAGGGGCAACTTTCTCTGGATTTTTGGCTTGGTTTGGTTGG  
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   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAGAGAATTTAGAGGCTGCCCACCGCCATTTTTCGCTTATTTGCCTAACGATTCTTATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTGGTTGG  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCTGAGGTTTTTTGGCTTGGTTTGGTTTGGTTGG  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCTGAGGTTTTTTGGCTTGGTTTGGTTTGGTTGG  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N N N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTCGCAGGCGATTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N N N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGACAGACTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTCCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGATTCTTAACGGTGTTGTT  1080 AGGGTGTTTTGATGGAATTTAGAGGCCATCTTAAAAAGAGTGGTTGATATTACAGAGCTTCGGTTGGTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N N N V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAGAGAACTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTCTGGATTGGTTTGCCTGAGGATGCTTAACAGGTGTTTTTTTT   
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  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 ITAGTTGGCTAAGCAGATTCTGAAGGCCTGCCCACCGCCATTTTTCGCTTATTTGCCTATGGGTTTGGTTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCCCCTATTTTTTATGACCTCATAGTTTTT 960  10 P D L N L E A 1 R R S L *  961 ITAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGCGCCAGTTCTATAACTTATAACGTGATGCTTTAAGGTGTTGTT 1080  AGGGGTGTTTTGATGACAACTTTAAGACGCCATTTTACAAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGGTTTTTTGGTGGGCTGACGGCCATGCAGATCCTAAA  1200 GAAATTGATGAGAATTTAAGGCAGACCTATTAGGGGGGAACTTTTTCGACGAGAATTTTTAAGACAAGTTTTTAAGACCATGCACCTGAATGAA   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V M W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCCCACTTTTTCCCTTATTTTGCCAGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTCTGAAGGCCTCCCCATTTTACTAAAAGAGTGGTTGATATTACAGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTAAAAAAAGAGTGGTTGATATTACAGCAGCTTCGCCTATTTTGGGTGGTTTTTTTGGGTGGCTGCTGAGCGCCATGCCAAGATCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAAGGCAAAACAGGTGTTACTAAAAAAAA  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCACCGCCATTTTTCGCTTATTTGCCAGGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGATATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCAATTTTACAAAAAAGAGTGTTGATATTACAGGCTTGCTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V M W H V V P S S S  Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 ITAGGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTGCCAGGGCAACTTTCTCTATAAACTTATAAGGTGACTGTTAAGGATGCTTAACGTATTTTCCCTAAGGGTGTTTT 1080  1081 AGGGGGTTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961
ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCGCTTATTTGCCAGGGGCTAACTTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTCTAGACGCCATTTTACTACAAAAGAGTGGTTGATATATACAGGCTTTGGGTTGGTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGGCTAAGGAGGGCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATGGTTTTT 960  I D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTCTGAAGGGCTGCCGCACTTTTACTACAGAGGTGTTGATTATACAGTATTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGGAATTTAGAGGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTGCCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGGCTAAGGAGGGCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATGGTTTTT 960  I D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGGAGATTCTGAAGGGCTGCCGCACTTTTACTACAGAGGTGTTGATTATACAGTATTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGGAATTTAGAGGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTGCCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATCTGAAGGGGTGCCCACCCCCCATTTTTCGCTTATTACCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATCTGAAGGGGTGCCCACCCCCCATTTTTCGCTTATTACCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTTATGACCTCATAGTTTTT 960  I D P D L N L E A 1 R R S L =  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTCCCAGCGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCCATTTTTCGCTTATTTCCCAGGGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCCATTTTTCGCTTATTTCCCAGGGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961
TTAGTTGGCTAAGCACATTCTGAAGGCCTGCCCACTTTTTCGCTTATTTTCCCAGGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  0861 M E F R R H F T T K E W L I L Q A S P I W Y G F L V A A A D G H A D P K  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGCTGCCACCCCCCATTTTTCGCTTATTTCCCAGGGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTTATGACCTCATAGTTTTT 960  I D P D L N L E A 1 R R S L =  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTCCCAGCGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R W W W V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTTATGACCTCATAGTTTTT 960  I D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTTTTCGCTTATTTCCCTATAGACTGTTATAACTTATAAGGTAGCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N N N V V P S S S  Element D -  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGGTTCGCAGGCCCCCCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTCTATAACTTATATAGGATGACTGTTACAGGTTCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACCAAAAGAGTGGTTGATATTACAGAGCTTGGGTTTGTTT  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G V N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAGAGAATTTAGAGGCTGCCCACCGCCATTTTTCGCTTATTTGCCTAACGATTCTTATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTGGTTGG  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCTATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATAGCCTCATAGTTTTT 960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  961 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCGCCATTTTTCGCTTGATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTCAGAGTACCTTAACGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGTTGG  
  | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCTATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATAGCCTCATAGTTTTT 960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  961 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCGCCATTTTTCGCTTGATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTCAGAGTACCTTAACGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N W N V V P S S S  Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCTATAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATAGCCTCATAGTTTTT 960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  961 AGGGGTGTTTTGATGGAATTTAGAGGCCGCACCGCCATTTTTCGCTTGATTTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTCAGAGTACCTTAACGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATCTAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGTTGG   | T Q R R L S Q L L R E L E L Y G L V E I E V V G R G R G R G R N N N N V V P S S S  Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGTAGTGAACTCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTCCCTTATTTTGCCAGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  |
| Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGAGTGAACTCCCCTATTTTTTATGACCTCATAGTTT  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTG  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT  | Element D .  GAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  P60  R S L *  CACCGCCATTTTTCGCTTGTTTGCCTGGATTTTTTGGTTGG  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGCTCATATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCACAGATCTTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTCCCTATGGGTTGATTTTTGCCTTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTAAAGAGTGGTTGATATTACAGGCTTCCCTATTTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTACAGTACCTCATGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCTAAGGATGACTGTTACAGGATGCTTACAGGATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGCTGTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTCCCCTATTTTGGTTGG  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 D P D L N L E A 1 R R S L *  961 TIAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTCCCTAGGGCCAACTTCTATAACTTATAAGGTGATGCTGTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACAAAAGAGTGGTTGATATTACAGCCCTATTTTGGGTTGGGTTTGTGGGTTGGGTTGTTTTTGGGTTGGGTTGTTTT  | Element D .
 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGCTCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGACAGTTCTGAAGGCCGCACCTCCCCCATTTTTCGCTAGGGCCACCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGCTCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGACAGTTCTGAAGGCCGCACCTCCCCCATTTTTCGCTAGGGCCACCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGAGAATTTAGAGGCCGCACCCCCCATTTTTCCCTAGTGTTATTACCTATAGACTGATTATTAACTTATAAGGTGATGTTTAAGGTGATCCTAAAGGTGTTGTT 1080  962 AGGGGTGTTTTGAGGAATTTAGAGGCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGCTCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGACAGTTCTGAAGGCCGCACCTCCCCCATTTTTCGCTAGGGCCACCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGAGCTCCTATTTTTTATGACCTCATAGTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGACAGTTCTGAAGGCCGCACCTCCCCCATTTTTCGCTAGGGCCACCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  
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   | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGAGAATTTAGAGGCCGCACCCCCCATTTTTCCCTTAGTTATTACCTATAGACTGATTATTAGAGTAGCTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGAGGAATTTAGAGGCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGAGAATTTAGAGGCCGCACCCCCCATTTTTCCCTTAGTTATTACCTATAGACTGATTATTAGAGTAGCTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGAGGAATTTAGAGGCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGAGAATTTAGAGGCCGCACCCCCCATTTTTCCCTTAGTTATTACCTATAGACTGATTATTAGAGTAGCTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGAGGAATTTAGAGGCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGAGAATTTAGAGGCCGCACCCCCCATTTTTCCCTTAGTTATTACCTATAGACTGATTATTAGAGTAGCTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGAGGAATTTAGAGGCCACTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  1  
  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 O P O L N L E A 1 R R S L *  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAAGAGTGGTTGATATTACAGCTTCGATTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 O P O L N L E A 1 R R S L *  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAAGAGTGGTTGATATTACAGCTTCGATTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAGACAGACTCTGAAGGGCTGCCCACCGCCATTTTCGCTTATTTCCCAGCGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGCCTTCGCCTATTTGGGTTGGTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TAGGTTGCTAAGGAACTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTCGCAGCGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCACCGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 O P O L N L E A 1 R R S L *  961 TTAGTTGGCTAGACAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATATAACTTATATGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAAGAGTGGTTGATATTACAGCTTCGATTGGGTTGGTT   
  | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TAGGTTGCTAAGGAACTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTCGCAGCGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCACCGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAGACAGACTCTGAAGGGCTGCCCACCGCCATTTTCGCTTATTTCCCAGCGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGCCTTCGCCTATTTGGGTTGGTT   | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGGTGAACTCCCTATTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCACAATTCTGAAGGGCTGCCACCCCCATTTTTCCCTAACGGGCAACTTCTCTGGATTTTTGCCTTAAGATGACTGTTACAAGAGTGTTTGTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT  
   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT  | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT  | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTATGACCTCATAGTTTTTT 960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCCACCGCCATTTTTCGCTTATTTCCCAGGGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTTGGTTGG   
   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTATGACCTCATAGTTTTTT 960  1 D P D L N L E A 1 R R S L =  961 TTAGTTGGCTAAGCACATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAACTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTTAGAGGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCTGCCCACCCCCCATTTTTCGCTTATTTGCCTAAGGATGATTTTTGCCTTAAGGATGATCCTTAAGGTTGTTT  1080 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTGGTTGG  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960 1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAGGGCTGCCCACCCCCCATTTTTCGCTTATTTGCCTAAGGATGATTTTTGCCTTAAGGATGATCCTTAAGGTTGTTT  1080 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTTGGTTTGGTTTGGTTGG  | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT  
                                       | Element D .  81 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCACTTTTTCCCTTATTACTATTAACTTATAAGTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGAGACGCCATTTTAGACGCCATTTTACTAAAAGATGGTTGATATTACTGCCATTTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTTAGTGAACTCCCTATTTTTTATGACCTCAAGGTTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCCACCGCCATTTTTCGCTTATTTGCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTCAGAGGCCATTTTACTACAAAGAGTGGTTGATATTACAGGCCTATTTGGGTTGGTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAGGAGGGCCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTCGCTCTGGTTGGT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCCTTATTTTCCCAGGGCAACTTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAGAGTGGTTGATATTACTGCCAGGCCTATTTTGGGTTGGTT   | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTTTTTTGCCTGAGTTTTTTATGACCTCATAGTTTTT  960  961 TAGGTTGGCTAAGCAGATTCTGAGGGCTGCGCACCGCCATTTTTCGCTTATTTTGCCAGGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTGCCTATTTGGGTGGTTTTTTTGGGTGCTGCTGACGGCCATGCCAGATCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAAAGAGTGGTTGATATTACAGGCTTTCGCCTATTTGGGTGGTTTTTTTGGGTGCTGCTGCCTGC  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTGATTTTTGCCTGTGATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTCTGAAGGCCACTCTTAACAAAAAAGTGGTTGATATTACAGCCTTCTATTTACCTTAACTTATAACTTATATAGGATGCTGCTGCTGACGGCCAGTCCTAAA  1081 AGGGGTGTTTTGATGGAATTTAAGGCCACCTTTTACTAAAAAAAA   
  | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTATGACCTCATAGTTTTTT 960  960 TAGGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCCCATTTTTCCCTTATTTGCCAGGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGGATGTCTTACCTAAGGGTGTTGTT  960 AGGGGTGTTTTGATGGATTTTAGAGGCCTGCGCACCCCATTTTACTACAAAAGAGTTGTTATTTGCCAGGCCATTTTTTTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCAAGGTTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCCACCGCCATTTTTCGCTTATTTGCCAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTCTAGAGCCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTGCCCTATTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCGCTTATTTGCCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCGCTTATTTGCCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCCCCCCATTTTTCCCTTATTTCCCTATGCCAGGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGAGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  1 D P D L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCCCCCCATTTTTCCCTTATTTCCCTATGCCAGGCCAGTTCTATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGAGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTCCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTGCCTGAGGTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCTCCTTTTTCCCTTATTTTCCCAGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT  
  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTGCCTGAGGTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCTCCTTTTTCCCTTATTTTCCCAGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGCCTGCCCACTTTTTCGCTTATTTCCCCTACTCTATTAACTTATAAGGTGATGCTTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTCTGAAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT  | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTGCCTGAGGTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCTCCTTTTTCCCTTATTTTCCCAGCGCAGTTCTATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGAATTCTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTCCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTGGGTTGGTT   | Element D >  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCCCTTATTTCCCTATGCGCCACTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGAGGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTTGGGTTGGTT   | Element D >  841
ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTCTCTGGATTTTTGCCTGAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTCCCTAGGGCCAACTTCTATAACTTATAACTTATATAGGATGACTGTTACCAGATTCTTTACCTAAGGGTGTTGTT 1080  961 TAGTTGGCTAAGCAGATTTAGAGGCCACCCCCCACTTTTTCGCTTATTACACTATAACTTATAACTTATATAGGTGTGTACCAGTTCTTAAGGGTGTTGTT 1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTACAAAAGAGTTGTAATATACAGACTTTTGGGTTGGGTTTGTTGGGTTGGGTTGTTTTGGGTGGGCCATGCAGGACCCTAAAA  1200 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGGGCAACTTTTTCGACGAGGATTTACCAAAGAAGTTTTTGAGGACCATGCACTGCACTGAATGACGATGCCCTATCTGCT 1320  E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGAGCCCCTTAGAGGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTCAAAGAATACATTACGTAATATGGCTTTTAAAATT 1440  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D +  841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGTTTTTTTT   | Element D .  841 ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGACTCCCTATTTTTTATGACCTCATAGTTTTT 960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCCACCGCCACTTTTTCCCTTGCCACCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  962 AGGGGTGTTTTGAGGAATTCTAGAGGCCACCGCCACTTTTTCCCTTATTACACTAATAACTTATATAAGGTGACTGTTACAGTACCTGAAGCGCCATGCAGATCCTAAA  1081 AGGGGTGTTTTGAGGAATTTAAGGCCACCATTTACAAAAAGAGTGGTTGATATTACAGGCTTTGGGTTTGGTTTTTTTT  |
| 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTT  1  | GAGGTCCCCTGAGGCTAACCTAGGGCAACTTICTCTGGATTITTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  R S L *  CACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  TACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGGATTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTCTATAACTTATAAGGATGACTGTTACAGGATCCTTACAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGACCCCATTTTACACAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGTTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1   |
ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG  
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT   
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTATTTCCAGGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTGATTTTTCCCAGGGCCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAAGTGACCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTGATTTTTCCCAGGGCCTTCGCCTATTTGGGTTGGTT  
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTATTTCCAGGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L **  961  1081  1081  1081  1081  1081  1082  1082  1083  1084  1085  1086  1086  1087  1087  1088  108 | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTGAGGGCAACCTTGCTGGATTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAAGGCCAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAAGGCCAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT 960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCCCTTATTTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  961 AGGGGTGTTTTGATGGAATTCAGAGGCTGCCGCACCGCCATTTTTCCCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGCTGCTGCTGCTGACGGCCATCCTAAA 1200  961 AGGGGTGTTTTGATGGAATTTAAGGGCGCCATTTTACTACAAAACAGTGGTTGATATTACAGGCTTGCTCTGTTTTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACCTTGCTGAGGCTATCTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961
ITAGTTGGCCTAAGCAGACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGCTGTTTTGATGGAATTCTAGAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCACAGAAGTTCTTTACAGTTTTTTTT   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCCCTTATTTTGCCAGCGCAGTTCTATAAACTTAATAAGTTAATAAGTTAACAGATTCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCTTATTTTCCCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGCTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAAAGATGGTTGATATTACAGGCTTCGCCTATTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCTTACTTA  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  960  960  961  960  961  961  962  963  963  964  965  965  966  966  967  967  968  968  968  968  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCCAACCTTCTCTGGGTTTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTGCCTAGGGCTAACTTCTATAACTTATAAGGAGAGAGTGTTACAGAATCTTAACAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCCATTTTCGCTTATTTGCCTACGGATGCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCCATTTTCGCTTATTTGCCTACGGATGCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCCATTTTTCGCTTATTTGCCAGGAGTGCTTATATATA   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCCATTTTTCGCTTATTTGCCAGGAGTGCTTATATATA   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTCTATATAACTTATATAAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TAGGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCAGATCCTAATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGGATCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  1081  1082  1083  1084  1085  1086  1086  1087  1087  1088  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAAGTGACCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAAGTGACCCCCTATTTTTTATGACCTCATAGTTTTT  960  961
ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGGATTTTTGCCTGAAGTGACCCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTCGCTTATTTGCCTGAGGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGATGGTTGATATTACAGGTTTTTTGGGTTGGTT  |
| 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTT  1  | GAGGTCCCCTGAGGCTAACCTAGGGCAACTTICTCTGGATTITTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  R S L *  CACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  TACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGGATTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTCTATAACTTATAAGGATGACTGTTACAGGATCCTTACAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGACCCCATTTTACACAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGTTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1   |
ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  1 0 P 0 L N L E A 1 R R S L *  960  961 TTAGTTGGCTAAGCAGTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTGTTTGGGTTGGGTTTTTTGGGTTGGTT   
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG  
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT   
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTCCCAGGGGCAACTTCTATAACTAATAAGGATGACTGTACAGTATCTTTACAGGGTGTTGTT  1081  AGGGGTGTTTTGATGGGATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTAGGTTTGGTTTGGTTTGGTTGG   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT   
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTATTTCCAGGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTGATTTTTCCCAGGGCCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGGATCTGAAAGGCTGCCACCCCCATTTTTCGCTTATTTCCCAGGGGCAACTTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTTATTTGGGTTGGTT  
  | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGGCAACTTTCTCTGGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTGATTTTTCCCAGGGCCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTTCCCAGGGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAAGGCCGCACCCCCATTTTTCGCTTATTTCCAGGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAGACACTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTTCCCAGGGGCAACTTTCTATAACTTATAAGGATGACTGTACAGGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG   
   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L **  961  1081  1081  1081  1081  1081  1082  1082  1083  1084  1085  1086  1086  1087  1087  1088
 1088  108 | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCCTGAGGGCAACCTTGCTGGATTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAAGGCCAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  AGGGGTGTTTTGATGGAATTTAAGGCCAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  10   
   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGCCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT 960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCCCTTATTTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080  961 AGGGGTGTTTTGATGGAATTCAGAGGCTGCCGCACCGCCATTTTTCCCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGCTGCTGCTGCTGACGGCCATCCTAAA 1200  961 AGGGGTGTTTTGATGGAATTTAAGGGCGCCATTTTACTACAAAACAGTGGTTGATATTACAGGCTTGCTCTGTTTTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACCTTGCTGAGGCTAACCTGGATTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCCTAAGCAGACTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGCTGTTTTGATGGAATTCTAGAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCACAGAAGTTCTTTACAGTTTTTTTT   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTGAGGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCCCTTATTTTGCCAGCGCAGTTCTATAAACTTAATAAGTTAATAAGTTAACAGATTCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCTATTTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCTTATTTTCCCTAGGGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGCTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAAAGATGGTTGATATTACAGGCTTCGCCTATTTGGTTGG   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTCCCTTACTTA   
  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  960  960  961  960  961  961  962  963  963  964  965  965  966  966  967  967  968  968  968  968  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCCAACCTTCTCTGGGTTTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTATTTGCCTAGGGCTAACTTCTATAACTTATAAGGAGAGAGTGTTACAGAATCTTAACAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCCATTTTCGCTTATTTGCCTACGGATGCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCCATTTTCGCTTATTTGCCTACGGATGCTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCACTTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCCATTTTTCGCTTATTTGCCAGGAGTGCTTATATATA   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCCCCCATTTTTCGCTTATTTGCCAGGAGTGCTTATATATA   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACTCCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTCTATATAACTTATATAAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 841 ATTGACCCTGACCTCATGCTTGAGGCCATAAGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  1 0 P 0 L N L E A 1 R R S L *  961 TAGGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCAGATCCTAATAACTTATATAGGATGACTGTTACAGATTCTTTACCTAAGGGTGTTTTT  1080  1081 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  |
ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961  1 0 P 0 L N L E A 1 R R S L *  961  1 TAGTTGGCTAAGCAGGATCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  1081  1081  1082  1083  1084  1085  1086  1086  1087  1087  1088  | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCTATTTTTTATGACCTCATAGTTTTT  960  961  TAGTTGGCCTAAGCAGCTCTGAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080  AGGGGTGTTTTGATGGGATTCTGAAGGCCTGCCACCGCCATTTTTCGCTTGATTTTCGCTTGGTTGG  | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGGCAACTTTCTCTGGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGGCAACTTTCTCTGGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGGCCATAAGGAGGTCCCTCTGAGGGCAACTTTCTCTGGGATTTTTTGCCTGAACTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 ITAGTTGGCTAAGCAGATTCTGAAGGGCTGCCGCACCGCCATTTTTCGCTTATTTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | ATTGACCCTGACCTCATGCTTGAGGCCATAAGGAGGTCCCCTCTGAGGCTAACCTAGGGGCAACTTTCTCTGGATTTTTGCCTGTAGTGACCTCCCTATTTTTTATGACCTCATAGTTTTT  960  961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTCGCTTATTTGCCTGAGGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTTTT  1080 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGATGGTTGATATTACAGGTTTTTTGGGTTGGTT  |
| 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTG 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | CACCECCATITITICECTTATTTECCAGCECAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  TACTACAAAAAGGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 961 TIAGTIGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTITTCGCTTATTTGCCAGGGCAGTTCTATATACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGATGGAATTTAGAGGCCCATTTTACTACAGAAGGTGGTTGATATTACAGGCCTTCGCCTATTTTGGGTTGGTT  | 17. TAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATATA  | 961 TTAGTTGGCTAABCABATTCTGAAGGCCTGCCACCCCCATTTTTCGCTTATTTGCCAGGCGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTAAAGAGTGGTTGATATTACAGCCCCCTATTTTGGTTGG  | 961
TTAGTTGGCTAAGCAGTTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  | 961 TTAGTTGGCTAAGCAGTTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 961 TTAGTTGGCTAAGCAGTTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  | 961 TTAGTTGGCTAAGCAGTTCTGAAGGGCTGCCACCCCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  
   | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 961 TIAGTIGGCTAAGCAGATIC TGAAGGGCTGCGCACCGCCATTITICGCTTATTTGCCAGGGCAGTTCTATATACTTATAGGATGACTGTTACAGTATCCTAAGGGTGTTGTT 1081 AGGGGTGTTITGATGGAATTTAGAGGCCATTTACTACAAAAGAGTGGTTGATATAACGCCTTCGCCTATTTTGGTTGG  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 961 TIAGTIGGCTAAGCAGATIC TGAAGGGCTGCGCACCGCCATTITICGCTTATTTGCCAGGGCAGTTCTATATACTTATAGGATGACTGTTACAGTATCCTAAGGGTGTTGTT 1081 AGGGGTGTTITGATGGAATTTAGAGGCCATTTACTACAAAAGAGTGGTTGATATAACGCCTTCGCCTATTTTGGTTGG  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG   
  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 961 TAGTIGGCTAAGCAGATTCTGAAGGCCTGCCCACCCCCATTITICGCTTATTTGCCAGGCCAG  | 1080 1081 AGGGGGTTTTTGAGGAGTTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGGTGTTTTGAGGAATTTAGGGCCAGCCATTTTACTACAAAGAGTGGTTGATATTACAGGCTTGCCTATTTGGGTTGGTT   | 1080 TAGTIGGCTAAGCAGATIC GAAGGGCTGCCCACCCCCATTITICGCTTATTTGCCAGGGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACAGAAAGAGTGGTTGATATAACTTATATAGGATGACTGTTACAGTATCTTACCGAGATCCTAAA 1200 CRF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCACCCTGAATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTTGGGGGAAGATCCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1440 CCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCTTGATGGGCAATTTAACTTTACCATTTACCTTTTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | 1740 1320 GAGATITAGACCCTTAGAGGGCACCCCCATTITAGGGCGGCAGCTCTATTACAGGAGTTCTATAACTTATAGGAGAGCTGTTACAGTATCTTACCTAAGGGTGTTGTT  1840 1320 GAGATITAGAGCAGATTTAGGGCGGCAACTTTTTCGAAAGAGTGGTTGATATACAGGCTTCGCCTATTTGGGTTGGTT   | 1080 1081 AGGGGGTTTTTGAGGAGTTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGGTGTTTTGAGGAATTTAGGGCCAGCCATTTTACTACAAAGAGTGGTTGATATTACAGGCTTGCCTATTTGGGTTGGTT  | 1080 1081 AGGGGTGTTTGAAGGCCTGCCCACCCCCATTTTCCCTTATTTCCCTACGCCAGTTCTATAACTTATAAGGAGAGCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTGAAGAACTGTTAAAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT   | 1740 1320 GAGATITAGACCCTTAGAGGGCACCCCCATTITAGGGCGGCAGCTCTATTACAGGAGTTCTATAACTTATAGGAGAGCTGTTACAGTATCTTACCTAAGGGTGTTGTT  1840 1320 GAGATITAGAGCAGATTTAGGGCGGCAACTTTTTCGAAAGAGTGGTTGATATACAGGCTTCGCCTATTTGGGTTGGTT   | 1080 TAGTIGGCTAAGCAGATIC GAAGGGCTGCCCACCCCCATTITICGCTTATTTGCCAGGGCAGTCCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGAGGAATTTAAGGCCCATTTTACAGAAAGAGTGGTTGATATAACTTATATAGGATGACTGTTACAGTATCTTACCGAGATCCTAAA 1200 CRF11 M E F R R H F T T K E W L I L Q A S P I W V G F L V A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCACCCTGAATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTTGGGGGAAGATCCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1440 CCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCTTGATGGGCAATTTAACTTTACCATTTACCTTTTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | 961 TIAGTIGGCTAAGCAGATIC TGAAGGGCTGCGCACCGCCATTITICGCTTATTTGCCAGGGCAGTTCTATATACTTATAGGATGACTGTTACAGTATCCTAAGGGTGTTGTT 1081 AGGGGTGTTITGATGGAATTTAGAGGCCATTTACTACAAAAGAGTGGTTGATATAACGCCTTCGCCTATTTTGGTTGG   | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT   | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 961 ITAGTIGGCTAAGCAGATICIGAAGGGCTGCCCACCGCCATITITCGCTTATTTGCCAGGCCAG   
  | 961 ITAGTIGGCTAAGCAGATICIGAAGGGCTGCCCACCGCCATITITCGCTTATTTGCCAGGCCAG  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGGATGATCATTAACTTAAGGGTGTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGAGAATTTAGACGCCATTTTACTAAGAGGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTTGGTTTGGTTTTTTTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGCCTGCCCCCCCATTTTTCCCTTATTTCCCAGCGCCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGAACTTTAGACGCCATTTTACACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG   | 961 TTAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTITTCGCTTATTTGCCAGCGCCAGTTCTATAACTTATAAGTGATGACTGTTACAGTATCTTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGAACTTTAGAGCCCCATTTTACAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  | 961 TTAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTITTCGCTTATTTGCCAGCGCCAGTTCTATAACTTATAAGTGATGACTGTTACAGTATCTTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGAACTTTAGAGCCCCATTTTACAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGTTGG  
   | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 961 ITAGTIGGCTAAGCAGATICIGAAGGGCTGCCCACCGCCATITITCGCTTATTTGCCAGGCCAG  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGGCGCAGTTCTATAACTTATAAGGTGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCCATTTTACTAAAAAAGAGTGGTTGATATTACAGGCCTTCGCCTATTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATTAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | P61 ITAGTIGGCTAAGCAGATTCIGAAGGGCTGCCCACCGCCATTITICGCTTATTTGCCAGGGGCAGTTCTATAACTTATAAGGTGATGATCACAGTTCTTACCTAAGGGTGTTGTT  1080 AGGGGTGTTTTGATGGAATTTAAAGGCCATTTTACAAAAAGGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTCGCTTATTTGCCAGGCGCAGTTCTATAACTTATAAGGTGGTGTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGACGCCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | 961 TTAGTTIGGCTAAGCAGATTCTGAAGGGCTGCCCCACTTTTTCGCTTATTTGCCAGCGCCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTAAAAAAAGTGGTTGATATTACAGCCAGC   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGAGCGCCATTTTACTACAAAAAGAGTGTTGATGTATATAACTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATATAAGTTATAAGTTATAAGTTATAAGTTATAAGTTATAAGTTATAAGTTATAAGGATGACTGCTGACGAGTCCTAAA 1200 1200 1200 1200 1200 1200 1200 1   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCCACCCCCATTTTCGCCTATTTGCCAGCGCAGTCTATATAACTTATAAGATGACTGTTACAGAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGATTTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCGCCATTTTTCGCTTATTTGCCAGGGGCTCTATATAACTTATATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGGTGGAATTTAGAGGCCAGATCCTAAA  080 ORF11 M E F R R H F T T K E W L I L Q A S P I W Y G F L Y A A A D G H A D P K  1201 GAAATTGATGAGAATTTAAGGCAGACCTATTTAGGGCGGCAACTTTTTCGACGGGTTTTTCCAAAGAGTTTTTTGAGGACCATGCACCCTGAATGATGACGATGCCCCTATCTGCT 1320   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGATGGAATTTAGAGCACACTCTAAAAAGAGTGGTTGATATTACAGGCTTGCCCTATTTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTTGATGGAATTTAGAGCACACTCTAAAAAGAGTGGTTGATATTACAGGCTTGCCCTATTTTGGGTTGGTT  | 961 TIAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTGCCCTATTTTGGGTTGGTT   
  | 961 TIAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTTGCCCTATTTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATATACAGGCCTTGCCCTATTTGGGTTGGTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGTGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATAATTACAGGCCTTGCCCTATTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGTGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATAATTACAGGCCTTGCCCTATTTGGGTTGGTT  | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATAATTACAGGCCTTCGCCTATTTGGGTTGGTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATAACTTATAAGTGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGGTGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATAATTACAGGCCTTGCCCTATTTGGGTTGGTT  
   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTTTTCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATATACAGGCCTTGCCCTATTTGGGTTGGTT   | 961 TTAGTTGGCTAAGCAGATTCTGAAGGGCTGCGCACCGCCATTTTTCGCTTATTTGCCAGGGCAGTTCTATATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 961 TTAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCACCCCCATTITTCGCTTATTTGCCAGGGCCAGTTCTATATACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCCTCCCCTATTTTGGGTTGGTT   | 961 ITAGTIGGCTAAGCAGATTCTGAAGGGCTGCCCCCCCATTITTCCCTTATTTCCCAGGCCAGTTCTATAACTTATAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGGAATTTAAGCCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTTGGGTTGGTT  | 1080 1081 AGGGGTGTTTGAAGGCCTGCCCACCCCCATTTTCCCTTATTTCCCTACGCCAGTTCTATAACTTATAAGGAGAGCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTGAAGAACTGTTAAAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT   | 1080 1081 AGGGGTGTTTGAAGGCCTGCCCACCCCCATTTTCCCTTATTTCCCTACGCCAGTTCTATAACTTATAAGGAGAGCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTGAAGAACTGTTAAAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT   | 1080 1081 AGGGGTGTTTGAAGGCCTGCCCACCCCCATTTTCCCTTATTTCCCTACGCCAGTTCTATAACTTATAAGGAGAGCTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1080 AGGGGTGTTTGAAGAACTGTTAAAGCCCATTTTACAAAAAGAGTGGTTGATATTACAGGCTTCCCCTATTTGGGTTGGTT   
   | 961 TIAGTIGGCTAGCAGATCTTGAAGGCCTGCCACCGCCATITITCGCTTATTTGCCAGCGCAGTTCTATATAACTTATAAGGATGACTGTTACAGTATCTTTACCTAAGGGTGTTGTT 1081 AGGGGTGTTTTGATGACACACCCCATTTTACACAAAAGATGGTTGATATTACAGGCTTGGCTATTTGGGTTGGTT   |
| 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | TACTACAAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1811 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1201  1202  1203  1204  1206  1206  1207  1208   | 1200  1201 
1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 
1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209 
1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 1200   12 | 1001 AGGGGGTTTTGATGGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTGCCTATTTGGGTTGGTT   | 1081 AGGGGTTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAAAGTGGTTGATATTACAGGCTTGGCTGATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
  | 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1200  1201  1202  1203  1204  1206  1206  1207  1208   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGGTTTTTGATGGAATTTAGACGCCAFTTTACTACAAAGAGTGGTTGATTACAGGCTTCGCCTATTTGGGTTGGTT  |
| 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | TACTACAAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1811 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1201  1202  1203  1204  1206  1206  1207  1208   | 1200  1201 
1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1209  1209  1209  1209  1200 
1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200 
1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209  1200   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | 1200  1201  1202  1203  1204  1206  1206  1207  1208  1209   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
  | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTTGGGTTGGTT   | 1200   12 | 1001 AGGGGGTTTTGATGGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTGCCTATTTGGGTTGGTT   | 1081 AGGGGTTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAAAGTGGTTGATATTACAGGCTTGGCTGATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
  | 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCAFTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  
   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | 1081 AGGGGTGTTTTGATGGAATTTAGAGGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT  | 1200  1201  1202  1203  1204  1206  1206  1207  1208   | AGGGGTGTTTTGATGGAATTTAGAGCCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   
   | AGGGGTGTTTTGATGGAATTTAGACGCCATTTTACTACAAAAGAGTGGTTGATATTACAGGCTTCGCCTATTTGGGTTGGTT   | AGGGGGTTTTTGATGGAATTTAGACGCCAFTTTACTACAAAGAGTGGTTGATTACAGGCTTCGCCTATTTGGGTTGGTT  |
| 1201 BAAATTGATGAGAATTTAAGGCABACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTG  | BBCGBCAACTTTTTCBACGBGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 AATFSTGFTKEVFEDHVYMHLNDDDALSA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1201 BAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | 1201 GAAATTGATGAGAAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | 1201
GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCCACTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTTGGGGAAAACTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 L Element D 1441 GCCCTTGTTTCTGATGGGAATCGAAGAGCGAAGAGCAGCTATCAAGTTGACTTTAACTTTAACTTTTCTTTTTTAAGGGGTGTC 1560  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTTGGGGAAAACTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 L Element D 1441 GCCCTTGTTTCTGATGGGAATCGATACAAGAGAGAAGAGCAGCTATCAAGTTGACTTTAACTTTAACTTTACTATTAACTTTTCTATTTAAAGGGGTGTC 1560   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTTGGGGAAAACTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 L Element D 1441 GCCCTTGTTTCTGATGGGAATCGATACAAGAGAGAAGAGCAGCTATCAAGTTGACTTTAACTTTAACTTTACTATTAACTTTTCTATTTAAAGGGGTGTC 1560   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTTGGGGAAAACTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 L Element D 1441 GCCCTTGTTTCTGATGGGAATCGATACAAGAGAGAAGAGCAGCTATCAAGTTGACTTTAACTTTAACTTTACTATTAACTTTTCTATTTAAAGGGGTGTC 1560  
  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTTCTGATGGGATGAGAAGAGAGAGAGAGAGAG   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  
   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTTCTGATGGGATGAGAAGAGAGAGAGAGAGAG  
  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTTAGAGGGGGTTTCTATTCTTTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 1440 L Element D 1441 GCCCTTGTTTCTGTGGGAATCGATAGAAGAGAGAGAGAGA  | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
   | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTAACTTTACTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTAACTTTACTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
  | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTAACTTTACTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1201 BAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCCACTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1201 GAAATIGATGAGAATITAAGGCARACTATTAGGGCGGCAACTITTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTTAAAAGGCGGTTTCATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4 Element D 4 Element D 5 CCCTTGTTTCTGATGGGAATGAGTGATTGACTTAACTTTACTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
  | 1201 BAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCCACTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTTCTGATGGGATGAGAAGAGAGAGAGAGAGAG  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   
   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGACCCCTTAGAGGCGGTTCTATACTTTTTTTT   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGACCCCTTAGAGGCGGTTCTATACTTTTTTTT   | 1201 BAAATTGATGAGAATTTAAGGCAGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCCCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | 1201 BAAATTGATGAGAATTTAAGGCAGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCCCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   
  | 1201 BAAATTGATGAGAATTTAAGGCABACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  | 1201 BAAATTGATGAGAATTTAAGGCABACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT  1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGACCCCTTAGAGGCGGTTCTATACTTTTTTTT   | 1201 BANATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGACGATGACCATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTAGAGCCCTTAGAGGCGGTTCTAATATTGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 L Element D 1441 GCCCTTGTTTCTGGTAGAGGAGACAGCAGAGAGAGAGAGA  | 1201 BAAATTBATGAGAATTTAAGGCAGCAACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGCACTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321
GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I   | 1201 BAAATTBATBAGAAATTTAAGBCAGACTATTAGGBCGGCAACTTTTTCGACSGGATTTACCAAAGAAGTTTTTBAGGACCATGCACTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  | 1201 BAAATTBATGAGAATTTAAGBCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGCCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1201 BAAATTBATBAGAACTATTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTAAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E 1 0 E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGAGCCCCTTAGAGGGGTTAAAGGCGGTTTCTAATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | BAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGCCCCTGAATGATGACGATGCCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGACCCCTTAGAAGGGGTTTCTAATGCTTTAAAAGTTCTATTCTTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320  
  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGCCACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320  |  |  | •   |  |   
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  | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A 1321 GTAGTAGAACCTTTAGAGGCGGTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 L Element D 1441 GCCCTTGTTCTGATGGGATGAGAAGGGGAAGAGAGAGAGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTBAGGACCATGCTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1201 BAAATTBATGAGAATTTAAGGCAGACTATTAGGGCGCAACTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACTGAATGACGATGCCCTATCTGCT 1320 E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGATTAAAAGGCGGTTTCTATTCTTTTTGGGGAAGATACCAGCTTCAGAAGGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  4 Element D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAACGAAGAGAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAGCAGTTGTCTTTTCAAGACAATTTTTTTT   |
|  | A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGAGCCCTTAGAGGGGTTAAAGGCGGTTCTATTCTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGSCTTTTAAAATT 1440 V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | E I D E N L
R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  
   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA  
  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   
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  |   |   |   | 1201 GAAATTGATGAGAATTTAAGGCABACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320   | 1201 GAAATTGATGAGAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTGAGGACCATGTCTACATGCACCTGAAYGATGACGATGCCCTATCTGCT 1320   | 1201 GAAATTRATRARAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGGCGGGATTTACCARACAAGTTTTTGAGGACCATGTGTGTACATGCACCTGAATGATGACATGCATCCCATGCATG  | 1201 CARATICATCACAATTIAACCCACACTATTACCCCCCAACTITITCCACCCCATTIACCAACACTITITCACCACCACTACATCACCACCACCACCACCACCACCACC  |   
  |  |  | 1201 GAAATTRATRARAATTTAAGGCAGACTATTAGGGCGGCAACTTTTTCGGCGGGGATTTACCABACAACTTTTTGAGGACCATGTCTACATGCACCCACCCCAGCCATGACCATGCATG   | 1201 BAAATTBATGAGAATTTAAGGCABACTATTAGGGCGGCAACTTTTTCGACGGGATTTACCAAAGAAGTTTTTSAGGACCATGTCTACATGCACCTGAATGATGACGATGCCCTATCTGCT 1320   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  
  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  |
|  | A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGAGCCCTTAGAGGGGTTAAAGGCGGTTCTATTCTTTTGGGGAAGATCCAGCTTCAGAAGCCGGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGSCTTTTAAAATT 1440 V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | E I D E N L
R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACTTGATGGGCAATTTAACTTTCATATTAACTTTTCTTTTTAAAGGGTGTC 1560  
   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA  
  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA   
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   | E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCAGCTATCAAGTTGATTGA  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   
  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACCTTAGAGCCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACCTTAGAGCCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACCTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   
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A E N F K D T L R N M A F K I   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACCTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGAGCCCCTTAGAGGGGTTTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGGAAAATTTCAAAAGTACATTACGTAATATGGCTTTTAAAATT 1440   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGAGGGGATTAAAGGGGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAAATTTCAAAAGTACATTACGTAATATGGCTTTTAAAATT 1440   | E I D E N L R Q T I R A A T F S T G F T K E V F E D N V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGGATTAAAGGGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGACCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | EIDEN LR QTIR AATFST GFT KEVFEDH VYMHL NDDDALSA  |   
  |   |   |   | 1201 BANATIBATOABARTITARBERBERBERALTITTICBALBBATTITACCAAAAATTITTBABBALBATATBICTACATGCACCAAAAATTACCATTACTACTATTACTACAATGCCCTAAAAAAAA  |  |   |  |   
  |  |  |   | 1201 BANATIBATOADANTITAABBEABEERITITABBEBBEARETTITTEBALBBATTTACEAAAAAA 1111BABBALBATATOAAA 16.CC IAAA 16.CC IIAAA 16.CC IAAA 16.CC I | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
  | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | E I D E N L R Q T I R A A T F S T G F T K E V F E D H V Y M H L N D D D A L S A  1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  |
|  |  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | 1321
GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 450 CCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGACTTAACTTAACTTTAACTTAACTTAACTTTTCTTTTTAAAGGGTGTC 1560  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 450 CCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGACTTAACTTAACTTTAACTTAACTTAACTTTTCTTTTTAAAGGGTGTC 1560  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 450 CCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGACTTAACTTAACTTTAACTTAACTTAACTTTTCTTTTTAAAGGGTGTC 1560  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 450 CCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGACTTAACTTAACTTTAACTTAACTTAACTTTTCTTTTTAAAGGGTGTC 1560   
  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   
   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA  
  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  
   | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  
  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTTTTT   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGTTTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | •  |   
  |   |   | FIJIFNIR DITTRAATEST GETKEVEED HVVM H 1 NDDDAISA  |  |  |   |  |   
  | 1201 BAAATTBATGAGAATTTAAGBCABACTATTABBBCGGCAACTTTTTCBACBBATTTACCAAAGAAGTTTTTBAGGACCATGCCCTGAATGATGACGATGCCCTATCTGCT 1320   | 1201 BAAATTBATBABAATTTAABBCABACTATTABBBCBCAACTTTTTCBACBBATTTACCAAAGAAGTTTTTBABBACCATGCCCGAATGACGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCGATGCATGC   |   |  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D   
  | 1321 GTAGTAGAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    4  |
|  | 1440 I TEABACTTTCACTECACATACCACACACACACACACACACACAC  |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | V V E T L D
P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  • Element D  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTCTTTTTTAAGGGGTGTC 1560   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  |  |  |  | 1444 TTASSTATASCATTASCATCASTASCASCASCASCASCASCASCASCASCASCASCASCASCA   |  
   |   |   |   |  |  | FIJIFNIR DITTRAATEST GETKEVEED HVYMH1NDDDAISA   |  |  
   |  | FIDENIR OTIRAATEST CETKEVEED HVVM HINDDDAISA   |   |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ## 1   |
|  |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  |   | ← Element D  | 4 Element D
1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT  | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT  | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT  | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTTT   | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTTT   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
   | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT  
  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT   | • Element D  | - Element D   | • Element D  | • Element D  
   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTTTTT   |   |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | Y V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   
  | V V F T I D D I F C I V A V C T I I C V T D A C F A F W F V D T I D M M A F V T  |  | 1501 OTENTEDESCONDETEDESCONDETEDESCONDETEDESCONDETEDESCONDETEDESCONDESCO |   |   |   |   
  | CINCHER GITK W WILD I PLIKE A LE NH A A W H C W N N D W C 2 N  | E JUEN LR QTIRA ATF STGFTKE V FEDH V Y M H L N D D D A L S A  | EIDEN LROTIRA ATFST GFT KEV FEDH V Y M H L N D D D A L S A   | EIDEN LR QTIR AATFST GFT KEVFEDH VYM HLNDDDALSA  | EIDENLR QTIRAATFS TG FTKEV FEDH V Y M H L N D D D A L S A  | EIDENLRQTIRAATFSTGFTKEVFEDHVYMHLNDDDALSA   
   | EIDEN LRQTIRAAT FST GFT KEV FEDH V Y M H L N D D D A L S A  |  | ← Element D  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | LETEMENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  |
| V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K  | KAVSILLGKIPASEAENFKOTLRNHAFKI  |  |   |  | 1441
GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTAACTTAACTTAACTTTAACTTTTCTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTAACTTAACTTAACTTTAACTTTTCTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   
   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA  |  |  
  |  |  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTCTTTTTAAGGGGTGTC 1560  | ◆ Element D  
  |  |  |  | ***************************************  | V V C T I D D I C C I V A V C T I I C V T D A C C A C W C V D T I D M M A C V T  |   
  |   |   |   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   
  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   |   
  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGCAGCATCATGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  |
| . Flement D  |  | <u> </u>   | ₄ Flement D   |  | 1441
GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTTAACTTGATGGCCAATTTAACTTACCATTTTAACTTTACTATTAACTTTCTTTTTAAGGGGTGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGGCAATTTAACTTACCATTTTACATTAACTTTACTTTTTAAAGGGTGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTAACTTAACTTAACTTTAACTTTTCTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTACAGTTTAACTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTAACTTAACTTAACTTTAACTTTTCTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATTGACCTTATACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGTGTC 1560   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   
  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA  |   
  |   |  |  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCTATCAAGTTGATTGA   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTCTTTTTAAGGGGTGTC 1560  | - Clamons o   | ₄ Flement ∩  | Flament O  |  |  | ***************************************  
   |  |   |   |   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  
   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   |   
  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTGATCGCCTTATACTTGACTTACCTATCTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGCAGCATCATGACCTTATACTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  |
|  | . Flement D  | 4 Floment D  |   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   |            
   | ALYSD G I DKNEEAAIKLI DLILD G QFNLPFYY*  | ALYSD GIDK NEEAAIKLIDLILD G Q F N L P F Y Y *  | ALYSD GIDKNEEAAIKLIDLILD GQFNLPFYY*  | ALYSD GIDK NEE AAIKLIDLILD G Q F N L P F Y Y *   
   | ALYSD GIDK NEEAAIKLIDLILD G Q F N L P F Y Y *  | ALV S D G I D K N E E A A I K Ł I D Ł I Ł D G O F N Ł P F Y Y *  | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY*   | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY *   
  | ALYSD GIDK NEEAAIKLIDLILD G QF NL P F Y Y *  | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY*   | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY*   | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY*   | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY*   | ALYSD GIDK NEE AAIKLIDLILD G Q F N L P F Y Y *   | ALYS D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   |   
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   |  |  | ······   |   | ······   
   | ······   |  | ALYSD G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | ALYSD G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | ALV SDGIDKNEEAAIKLIDLILDGQFNLPFYY *   
  | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ALY S D G I D K N E E AAIKLIDLILD G Q F N L P F Y Y *   |   | **** ASSESSED TO A SECOND CONTRACT OF THE PROPERTY OF THE PROP | 1941 GULUTTOTTUTOR TOGRATUGA FRARACIGA GAGGAGUTA TURAGITIGA TIGACUTTA FOLITI TIRAGITA CONTRACTA | TATE ARREST TO THE TATE OF THE PARTY OF THE  |  |   
  | ALV S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | ALYSD 6 I DK MEEAAIKLIDLILD G QF NLPFYY*  |   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTAACTTTTAACTTTTTTTAAGGGGTGTC 1560   |  |  | ₄ Flowert ∩  | Flement D  
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   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAGGCATTGACTTGACCTTATACTTTGATGGGCAATTTAACTTTCACATTTTACTATTAACTTTCTTT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACCTATTTACTATTTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC  1680   | LE Pement D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAAGAAGCAGCTATCAAGTTGACTTACCTTATACTTTACCATTTTACCATTTTACCTTTTACCATTTTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTAATGTCCTATGGGTCGGC 1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAGGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGCAGCTATCAAGTIGATTGACCTTATACTTTAACGTTTAACTTTAACTTTTAATTAA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGCAGCTATCAAGTIGATTGACCTTATACTTTAACGTTTAACTTTAACTTTTAATTAA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  440  4  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   
   |  |  |  |  | AGE AGAITTECCONTRACTORACTORACTORACTORACTORACTORACTORACT  |
|  | AGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  AGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTAGGTAATGTCCTATGGGTCGGC  1680  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTCTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680  |            
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   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACATTGTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGCATATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGGTCC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAGGAAGAAGGAGCAGCTATCAAGTTGATTGA   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGCAGCAAGAGAGAG  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGGAGGAGGAGGTATCAAGTTGATGACCTTATACTTACACTTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC  1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAAGAGGAGGAGGAGGTATCAAGTTGATGACCTTATACTTACACTTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC  1680  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGGCGGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGGTTGATGACCTTGATGGGCAATTTAACTTTAACTTTTCTTTTTAAAGGGTGTC  1560 TGAGGGTTTGCCCCGTAATCTTCCTGAAGGCAGCAATTGTCTTTTCAAGACAATTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT   1440   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680  
   |  |  |  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGCCACCACGGGGGGCTACCGCCCCCCCC  | ***  |
| IR1' 4   | AGAAGCAGCTATCAAGTTGACTTGATCTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAGGAGCTATCAAGTTGATTGA   | A L V S D G I D K M E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1' 4     
   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4   | IR1' 4   
   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4IR2'4  1681 TAAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC  | IR1' 4   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT   
  | IR1' 4   | IR1' 4   | IR1' 4   | IR1' 4   | IR1' 4IR2'4  1681 TAAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC  
   | IR1' 4   | IR1' 4   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  |   
   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4IR2'4  1681 TAAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC   | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   
  | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTSTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  1680   
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4  | IR1' 4   
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGAAGAGAGAG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGATACAAGTGATTGACCTTATACTTGATGGGCAATTTAACTTTAACTTTTCTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1441 GCCCTTGTTTCTGATGGGATCGATAAAAAGGAGGAGCAGCTATCAAGTTGATTGA   | Element D  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCAACAGAGTGACATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 2 1 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2   
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 2 1 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I 2 1 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
  | IR1' 4IR2'4  1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   |  |  |
| 1811 1R11 1R11 1R11 1R11 1R11 1R11 1R11  | AGAAGCAGCTATCAAGTTGACTTGATCTTGATGGGCAATTTAACTTTCACTATTAACTTTTCTTTTTAAGGGGTGTC  E A A I K L I D L I L D G Q F N L P F Y Y *  AGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680  TCGCTCGGCTCGGAAATCGCCGCCGACCAGGGGGGGCTAACCGCCCCCCCC  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K M E E A A I K L I D L I L D G Q F M L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 181' 4     
   | 181' 4   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 181' 4   | 181' 4   
   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 181' 4   | 181' 4   | 181' 4   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC   
  | 181' 4   | 181' 4   | 181' 4   | 181' 4   | 181' 4   
   | 181' 4   | 181' 4   | 181' 4   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | IR4'  
   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 181' 4  | 1R1' 4   
  | 1R1' 4   | 1R1' 4   | 1R1' 4   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1R1' 4   | 1R1' 4   | IR1' 4  | IR1'IR2'4 1881 TAMECGATTTCCGCCCTTTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC  
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCCGCCCCCCCC  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1660 | 1681 TAAGGATTTCGCCCCTTTCGGGGCCCCCCCCCCCCCCCC   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | Element D  
   | LETEMENT D  LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LETEMENT D  L | 2 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1R1' 4   
   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | IR4'   | IR4'   |
| 1R1' 4   | AGAAGCAGCTATCAAGTTGATTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  E A A I K L I D L I L D G Q F N L P F Y Y *  AGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680  TCGCTCGGCTCGGAAATCGCCGCCGACCAGGGGGGGCTAACCGCCCCCCCC  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 181' 4     
   | 181' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 181' 4   | 181' 4   
   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 1R1' 4   | 181' 4   | 181' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC   
  | 181' 4   | 181' 4   | 181' 4   | 181' 4   | 1R1' 4   
   | 181' 4   | 181' 4   | 181' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC   
  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | IR4'  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGCC   
  | 1R1' 4  | 1R1' 4  | 1R1' 4   | 1R1' 4   | 1R1' 4   
                 | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTAATGTCCTATGGGTCCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  
  | 1R1' 4   | 1R1' 4   | IR1' 4  | IR1'IR2'4 1R8' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTAGGTAATGTCCTATGGGTCGGCCCCCCCC   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCGTTGGTTG  | 1660  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCGAGGGAGCAGCTTGCTT  | 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGCTTTTTCAAGACAATTTTTTTT                
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | Element D  | 1441   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEMENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGGTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGGTATCAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441
GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1R1' 4   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   | IR4'   
   | IR4'   |
| IR1'  TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   | AGAAGCAGCTATCAAGTTGACTTGATCTTGATGGGCAATTTAACTTTCACTTTTAACTTTTCTTTTTAAGGGGTGTC  E A A I K L I D L I L D G Q F N L P F Y Y *  AGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680  TCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  | 1560  1660   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1'       
   | IR1'   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGG   | IR1'   | IR1'   
   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGG   | 1801 TITTETEGRATTTACCCCTTCACCCCGACACTCTTATATAGACGCCAGCTTCETCAGTTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCCAGCTTCGTTCG  | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGG  
  | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 1801 TITTETEGRATTTACCCCTTCACCCCGACACTCTTATATAGACGCCAGCTTCETCAGTTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCCAGCTTCGTTCG  
   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 181 TAAGGATTTCCGCCCTTCGGGTCGCTCGCTCGGCCGACACGGGGGGGTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGG   | 1801 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCCGGCGGGGGGGCTACCGCCCCCCCC  
  | 1801 TANGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGTACCGCCCCCCCC  | 1801 TTTTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT  | 1801 TANGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGTACCGCCCCCCCC  | 1801 TANGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCAGGGGGGGTACCGCCCCCCCC  | 1801 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCCCGGCCACCCGGCGGGGGGGCTACCGCCCCCCCC  
  | 1801 TITTETEGRATTTACCCCTTCACCCCGACACTCTTATATAGACGCCAGCTTCETCAGTTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCTCGTTCTATATAGACGCCAGCTTCGTTCG   | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG   | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  
                 | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACCTCTTATATAGAGGCCAGCTTCGTCAGTTCGTCAGCTTCGCTCGC  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGCCCCCCCC  | TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680  | TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680   
  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG   | 1801 TITTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTGGTCAGTTATATAGAAGGTAACGCTCGCT  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680   | 1561 TGAGGGTTTGCCCCGTAATCTCCGACCCCGACACTTGCTTTTCAAGACAATTTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGCATTCAAGTTGATTGA   
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | Letement D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 2 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAAGC  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAATCA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAATCA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | GCCCTTGTTTCGATGGAATCGATAAAAGCGAAAGCAGGTTCAAGATGGCAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LEMENT D  LEMENT D  LEA V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y **  LEA A I K L I D L I L D G Q F N L P F Y Y **  LEAGAGGTTTGCCCCGTTAGGGTAGGTCGCTCGGTTGGTAAGCAAAGTTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   
  | GCCCTTGTTTCGATGGAATCGATAAAAGCGAAAGCAGGTTCAAGATGGCAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LEMENT D  LEMENT D  LEA V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y **  LEA A I K L I D L I L D G Q F N L P F Y Y **  LEAGAGGTTTGCCCCGTTAGGGTAGGTCGCTCGGTTGGTAAGCAAAGTTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | TRANSCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACTCCGTCTCGCTCG  | 1801 TTTTGTGCATTTACCCCTTCACCCCGACACTCTTATATAGAGGCCAGCTTCGTCAGTTATATAGAGGCCAGCTTCGTTCG  | 1801 TANGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGTACCGCCCCCCCC  | 1801 TANGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGTACCGCCCCCCCC  | 1801 TTTTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGATTCGCTCGC   
  | 1801 TTTTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT   |
| 1881 TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC   | AGAAGCAGCTATCAAGTTGATTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  E A A I K L I D L I L D G Q F N L P F Y Y *  AGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  L680  IR4'  CACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAGTTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGCTCTGGCTTGGTAATGTCCTATGGGTCGGC 1680  1801 TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGCTCGGCAGCAGCCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1881
TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1801 TATAGTACTATAGAGGACTTCCCCCCGCCCCGCCCCCCCC  | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  
  | 1801 TATAGTACTATAGAGGACTTCCCCCCGCCCCGCCCCCCCC  | 1881 TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1801 TATAGTACTATAGAGGACTTCCCCCCGCCCCGCCCCCCCC  
   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  
  | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTCGGGCCCCCGGCACACTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1801 TATAGTACTATAGAGGACTTCCCCCCGCCCCGCCCCCCCC  | 1801 TATAGTACTATAGAGGACTTCCCCCCGCCCCCCCCCCCC   
   | TAMAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCACCCCCCCC  | TAMAGGATTTCCGCCCTTCGGGTGGCTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCACCCCCCCC   | 1801 TITTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT  | 1801 TATACTARAGGATTTCCGCCCTTCGCTGGCTGGCTGGCTCGCTCGGCCGCCG  | TAMAGGATTTCCGCCCTTCGGGTGGCTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCACCCCCCCC   
   | TAMAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCACCCCCCCC  | 1881 TAAGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC  
  | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4  | IR1' 4  | TATAATACTAABAGGTATGACGAAGCTGGCGTGAATTATTTTGAGGGCTCGCTC   | TATAATACTAAGAGGATTGACGAGGAGCAGGGGGGGAATTATTTTGAGGGCTCGGCTGGAAGAGGGGGGGTGAATGACGAGGGTCGCTCGGAAGGGGTGAATGACGAAGAGTCCTTA  TGAGGGTTTGCCCCCGTAATCTTCCTGAAGTGCAGCAGTTGTTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | TATATACTAAGAGGTATGCCCGGAATCTTCCTGAAGTGCAGCATTATTTTTGAGGGCTCGGCCCGGCCCGCGCCCCCACCTCGGCTTGGTAAGTCCTATGAGTCCTTAGGTCGCCCCTTCGCTCGC   
   | TATATACTAAGAGGTATGCCCGGAATCTTCCTGAAGTGCAGCATTATTTTTGAGGGCTCGGCCCGGCCCGCGCCCCCACCTCGGCTTGGTAAGTCCTATGAGTCCTTAGGTCGCCCCTTCGCTCGC   | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4  | IR1'  1681 TAMGCGATTTCCGCCCTTCGGGTCGCTCGCTCGGCAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680 IR1'   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
  | 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGGGCACACTTGCTTTTTCAAGACAATTTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | * Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTTACCTATACTTGACCTTTTACCTTTTACCTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTTACACTTTTACACTTTTTACACTTTTACACTTTTACACTTTTACACTTTTACACTTTTACACTTTTACACACTTTTACACACTTTTACACACTTTTACACACTTTTACACACTTTTACACACTTCGACACTTCGACACTTCGACACTTTTACACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACTTCGACACACCCCCCCC   | LETT L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I   | 2 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAATGTGATGGGCAATTTAACTTAACTTTAACTTTTAACTTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAGACACACTTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGAAGATTATTAACTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAAACTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGAAGATTATTAACTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAAACTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.   | GCCCTTGTTTCTGATGGAACCTTAAAAGGGATGAAAAGGAAGAAGAGAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LEMENT D  LEMENT D  LEL G K I P A S E A E N F K D T L R N H A F K I  CENNENT D  LA V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y 2  LEAGAGGATTTCCCCCCGTAATCTTCCTGAAGGGAACCACCATTGTTTTTTTT   | GCCCTTGTTTCTGATGGAACCTTAGAGGGATGAAAGCAGGGTTCTATTCTTTTGGGGAAGATCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LET CONTROL CON | GCCCTTGTTTCTGATGGAACCTTAGAGGGATGAAAGCAGGGTTCTATTCTTTTGGGGAAGATCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LET CONTROL CON | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I 1440 CCCCTTGTTTCTGATGGGATCGATAAAAAGCGAAAGCAGGCTATCAAGTTGATTGA  | GCCCTTGTTTCTGATGGAACCTTAGAGGGATGAAAGCAGGGTTCTATTCTTTTGGGGAAGATCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LET CONTROL CON | GCCCTTGTTTCTGATGGAACCTTAAAAGGGATGAAAAGGAAGAAGAGAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  LEMENT D  LEMENT D  LEL G K I P A S E A E N F K D T L R N H A F K I  CENNENT D  LA V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y 2  LEAGAGGATTTCCCCCCGTAATCTTCCTGAAGGGAACCACCATTGTTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1811 TAAGCGATTTCCGCCCTTCGGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | 1801 TATACTARAGGATTTCCGCCCTTCGCTGGCTGGCTGGCTCGCTCGGCCGCCG  | 1801 TATACTARAGGATTTCCGCCCTTCGCTGGCTGGCTGGCTCGCTCGGCCGCCG  | 1801 TITTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCATATATACGAAGTAACGCTCGCT  | 1801 TITTGTGCATTTACCCCTTCACTCCACCCCGACACTCTTATATAGACGCCAGCTTCGTCAGTACCTCGTATTATACGAAGTAACGCTCGCT   |
|  | AGAAGCAGCTATCAAGTYGATTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCGACTTATACTTGATGGCCAATTTAACTTACCTATCAATTTAACTTTCTTT   |   |  | A C T S D D
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   |  | 1201 IBAGGGTTGCCCCGTAATCTTCCTGAAGTGCATCGTCTTTCAAGACAATTTTTTGGCCAAAAGTGTTGGTGGCTTGGCTTGGCAAGTGCCTATGGCCGC 1000  | 1501 ISASSITISCCCGIANICITCCIANGIBLASCATISITITICAAACAATTIIIIIGGICAAAAASITIIIIGGICIIIGGIIIGGIIIGGIAATGICCIAIGGCICGC 1000   | 1501 ISASSETTSCCCCGTARTCTCCTSARGTSCRETTSTCTTTCAAGACAACTTTTTGCCCAAAAGTGTTTTGGTCAAAAGTGTTTGGTTGG   | 1501 ISASSETTSCCCCGTARTCTCCTSARGTSCRETTSTCTTTCAAGACAACTTTTTGCCCAAAAGTGTTTTGGTCAAAAGTGTTTGGTTGG  
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  |  | •   | A C T S D G I D K H C C A A I K C I V C I C U G Q I N C F I I I   | A   V   |  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCATTTTACCTTATCACTTTTACTATTAACTTTTCTTTTTAAAGGGGTGC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTCTTTTTAAGGGGTGTC 1560   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGGAGCTATCAAGTTGATTGA   
   | Clement D  1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTGAC  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGGAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I - Element D 1441 GCCCTTGTTTCTGATGGGATCGATAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I - Element D 1441 GCCCTTGTTTCTGATGGGATCGATAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA  
   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGAGAGCAGCTATCAAGTTGATCTGATGGGCAATTTAACTTTTACTATTAACTTTTTTTT   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGAGAGCAGCTATCAAGTTGACCTTTATACTTTAACTTTTAACTTTTAACTTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 2 Element D 1441 GCCCTTGTTTCTGATGGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGATCTGATGGGCAATTTAACTTTTCTTTTTTAAGGGTGTC 1560  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 440 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGAGAGCAGCTATCAAGTTGACCTTTATACTTTAACTTTTAACTTTTAACTTTTTTTT   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG  
   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I - Element D 1441 GCCCTTGTTTCTGATGGGATCGATAAAACGAAGAAGAGCAGCTATCAAGTTGATTGA  | 8   V S D G T D V M C C A A T Y I T D 1 T I D C O C M 1 D C V V *  | •••••  | プロスト   プロストース・ファース・ファース・ファース・ファース・ファース・ファース・ファース・ファ  |  | 1301 Indiana i indecetta inni enterta inni enterta inni enterta inni indi enterta indi inni enterta indi ente |  |
|  | AGAAGCAGCTATCAAGTTGATTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  1560  E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAGGAGCATATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   |            
   |  | 101'   |  |  
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   |  |  |  | 101'   | 101'  
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCAGCIATCAAGTTGATCTTGATGGGCAATTTAACTTTCACATTTTAACTTTCTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATGACCTTATACTTGATGGGCAATTTTACCTATTTACTATTTAACTTTTCTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCATTGGCTCTGGCTTGGTAATGTCCTATGGGTCGCC  1680  | LETEMENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTTAACTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTAACTTTAAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAAACTTAAACTTAAACTTAAACTTAAACTTAAACTTAAACTTAAAAAA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCATTATCATTGATGGGCAATTTAACTTTCATTTAACTTTCATTTTAACGAATTTTAACTTTTCATTTTAACGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCATTATCATTGATGGGCAATTTAACTTTCATTTAACTTTCATTTTAACGAATTTTAACTTTTCATTTTAACGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1440 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  
   |  | 191'   | 101'   |  |  |
|  | AGAAGCAGCTATCAAGTTGATTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC  1560  E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAGGAGCATATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   |            
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCAGCIATCAAGTTGATCTTGATGGGCAATTTAACTTTCACATTTTAACTTTCTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCIATCAAGTTGATGACCTTATACTTGATGGGCAATTTTACCTATTTACTATTTAACTTTTCTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCATTGGCTCTGGCTTGGTAATGTCCTATGGGTCGCC  1680  | LETEMENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGACCTTATACTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTTAACTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTAACTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTAACTTTAAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAACTTTAAACTTAAACTTAAACTTAAACTTAAACTTAAACTTAAACTTAAAAAA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCATTATCATTGATGGGCAATTTAACTTTCATTTAACTTTCATTTTAACGAATTTTAACTTTTCATTTTAACGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAGCATTATCATTGATGGGCAATTTAACTTTAACTTTCATTTAACTTTCTTT  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E I L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
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   |  |  |  |  | 1881 TARGOGATTICOSCICCTTTOGGGTOGCTTCGCTTCGCTCGCTCGCTCGCCCGCC   |
| IR1' 4IR2'4  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC  |            
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTGACCTCTGGCTAATGTCCTATGGGTCGGC  1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAGAGAGAG  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAACTTGTCCTATGGGTCGC  1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  
   |  |  |  | 1601 TBSCCCSTTTCCACACTTTACACATTACACTTACACTTACACTACACTCCCCCC  | - 400 L   1880 LONG  |
| IR1' 4IR2'4  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC  |            
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   |  |  |  | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT   |  
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTGACCTCTGGCTAATGTCCTATGGGTCGGC  1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAGAGAGAG  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAACTTGTCCTATGGGTCGC  1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAAGAGAGAG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  
   |  |  |  | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  |  |
|  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAGAGAGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | IR1' 4IR2'4
   | IR1' 4IR2'4  | •  | IR1' 4IR2'4  | IR1' 4IR2'4  
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  | •  | 1681 TAAGCGATTTCCGCCCTTTCGGCTCGCTCGCTCGCTCGCAACTGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC  | •  | •  | •   
  | IR1' 4IR2'4   | IR1' 4IR2'4   | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4  
                 | IR1' 4IR2'4   | IR1' 4IR2'4   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  
  | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   
  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'   | IR1' 4IR2'4  | •  | •  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTTCGCTCGGTCGG   
  | 700 1110001110000000111000100010010000000  |
IR1' 4IR2'4	AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *	1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGATTGA	A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG	1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC
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   |  |  |  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   |  
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTGACCTCTGGCTAATGTCCTATGGGTCGGC  1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAGAGAGAG  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAACTTGTCCTATGGGTCGC  1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  
   |  |  |  | 1681 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTTCGCTCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC  | TOTAL TRANSPORT TO THE PROPERTY OF THE PROPERT |
| IR1' 4IR2'4  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAAGCAGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC  |            
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  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC   
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAAFTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTGACCTCTGGCTAATGTCCTATGGGTCGGC  1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAGAGAGAG  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAACTTGTCCTATGGGTCGC  1680   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATGGATAGAAGAGAGAGAGAGA   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT  V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  4. Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGAGAG   | 1321 GTAGTAGAAACTITAGACCCCTTAEAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  
   |  |  |  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   |  |
| IR1' 4   | AGAAGCAGCTATCAAGTTGACTTGATCTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTCTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGGAGGAGCTATCAAGTTGATTGA   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCACTTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1' 4IR2'4
 1681 TAAGGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCACCCCCCCC  | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4   | IR1' 4   
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  | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  |   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT   
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   | IR1' 4   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | IR1' 4   | IR1' 4   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCGTCGGCTTGGTAATGTCCTATGGGTCGGC 1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGATACAAGTGATTGACCTTATACTTGATGGGCAATTTAACTTTAACTTTTCTTTTTTAAGGGGTGTC  1560  A L V S D 6 I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAAGAGAGCATTCTATACTTGATGGGCAATTTAACTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAAGAAGAAGAAGAAGATTAACTTAACTTAACTATTAACTTTTTTTT  | Element D  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCAGTACAAGTTGACCTTATACTTTAACTTTTAACTTTTAACTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAACTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441
GCCCTTGTTTCTGATGGATGGATGGATGAGAGGAGGAGGAGGTGAGGTGATTGACTTTACTATTACTTTTTCTTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGATGGATGGATGAGAGGAGGAGGAGGTGAGGTGATTGACTTTACTATTACTTTTTCTTTTTTAAGGGGTGTC  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 CCCTTGTTTCTGATGGGAATCGATGAAAAAGGAAGAAGCAGGTTCAAAGTGATTGACCTTTAAATTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y 2 11561 TGAGGGTTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 CCCTTGTTTCTGATGGGAATCGATGAAAAAGGAAGAAGCAGGTTCAAAGTGATTGACCTTTAAATTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y 2 11561 TGAGGGTTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321
GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 CCCTTGTTTCTGATGGGAATCGATGAAAAAGGAAGAAGCAGGTTCAAAGTGATTGACCTTTAAATTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y 2 11561 TGAGGGTTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   
   |  |  |
| IR1' 4   | AGAAGCAGCTATCAAGTTGACTTGATCTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTCTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1560  1660  | A L V S D G I D K N E E A A I X L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGGC  1680   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1' 4IR2'4
 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGGCTACCGCCCCCCCC   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4   | IR1' 4   
   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4   | IR1' 4   | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT   
  | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  |   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT   
  | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCT  | IR1' 4  | IR1' 4  | IR1' 4   | IR1' 4   
   | IR1' 4   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   
  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC  | IR1' 4   | IR1' 4   | IR1' 4  | IR1' 4  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCGTCGGCTTGGTAATGTCCTATGGGTCGGC 1680   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGATACAAGTGATTGACCTTATACTTGATGGGCAATTTAACTTTAACTTTTCTTTTTTAAGGGGTGTC  1560  A L V S D 6 I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAAGAGAGCATTCTATACTTGATGGGCAATTTAACTTTAACTTTTAACTTTTAACTTTTTAACTTTTTAACTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAAGAAGAAGAAGAAGATTAACTTAACTTAACTATTAACTTTTTTTT  | Element D  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCAGTACAAGTTGACCTTATACTTTAACTTTTAACTTTTAACTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAACTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441
GCCCTTGTTTCTGATGGAATGATAAAAAGGAGAAGAAGGAGGTGATCAAGTTGATGACCTTATACTTTAACTTTTCTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATGATAAAAAGGAGAAGAAGGAGGTGATCAAGTTGATGACCTTATACTTTAACTTTTCTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321
GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTACTATTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTAICAAGTTGATTGACCTTATACTTTAACTTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCAATTTTTCAAGACAATTTTTTTT   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCCCCCCCC  | IR1' 4   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   | 1881 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCCCC   
   |  |  | | | |
| IR1' 4IR2'   | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGAGGAGGCTATCAAGTTGATTGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |            
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   |  |  |  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTTCGCTCGC   |  
   |  |  |   |   |   
  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680   |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680  
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAGAGAGAGAG  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAGCTTGGTTGACCTCTGGTAATGTCCTATGGGTCGC  1680  | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAGCTTGGTTGACCTCTGGTAATGTCCTATGGGTCGC  1680  | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAAGGAGGAAGAGGCATGAAGTGATGAACTTGATGGGCAATTTAACTTTACATTTAACTTTTCTTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGTTAGCTTGGTTGACCTCTGGTAATGTCCTATGGGTCGC  1680  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N N A F K I  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAACCTCTGGGTCGGC 1680   
   |  |  |  | 1881 TANGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   |  |
|  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGGATCGATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  |            
   | IR1' 4IR2'4  | •  | IR1' 4IR2'4  | IR1' 4IR2'4  
   | •  | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4  | •   
  | IR1' 4IR2'4  | •  | •  | •  | •  
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  | •  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC  | •  | •  | •   
  | IR1' 4IR2'4   | IR1' 4IR2'4   | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4  
                 | IR1' 4IR2'4   | IR1' 4IR2'4   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   
  | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4   | IR1' 4IR2'4   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTTTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGGATCGATACAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1441 GCCCTTGTTTCTGATGGGATCGATACAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA  | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA  | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441
GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680  | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   | 1321 GTAGTAGAAACTITAGACCCCTTAGAAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440    • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAGGGGGTATCAAGGTGATTGACCTTATACTTGATGGGCAATTTTACCTTTTTAACTTTTCTTTTTAAGGGGTGTC 1560    • A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCACCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680   
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGTACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 CCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGAAGTTAACTTTACTATTAACTTTTCTTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCASCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680 CCCCTTGTTTGACCTCTGGAAGTGCAAGAGTGCAAAAAGTTGTTTTTTTT   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGGATTAAAAGGGGGTTCTATTCTTTTGGGGAAGGTACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I 1440 CCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGAAGAAGAAGTTAACTTTACTATTAACTTTTCTTTTTAAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCASCATTGTCTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGCTTGGTAATGTCCTATGGGTCGCC 1680 CCCCTTGTTTGACCTCTGGAAGTGCAAGAGTGCAAAAAGTTGTTTTTTTT  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG  | IR1' 4IR2'4  | •  | •  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGGAAATCGCCGCCGACCAGGGGGGCTACCGCCCCCACCCCCCCC   
   | The state of the s |
IR1' 4IR2'4	AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *	1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA	A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG	1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAATGTCCTATGGGTCGGC  1680  IR1'
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   |  |  |  | 1681 TAAGCGATTTCCGCCCTTTCGGGTCGCTCGCTCGCTCGCACCACCCCCGCCCACCCCCCCC  |  
   |  |  |   |   |   
  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  1680  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  1680  IR1'  |  |  |   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  1680  IR1'   
   | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCAGCTATCAAGTTGATCTTTAACTTTAACTTTAACTTTTAACTTTTAACTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGCAGCTATCAAGTTGATCTTTAACTTTAACTTTAACTTTTAACTTTTAACTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   
   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATGACCTTATACTTAACTTTAACTTTAACTTTTAACTTTTAAAGTGTTCTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATGACCTTATACTTAACTTTAACTTTAACTTTTAACTTTTAAAGTGTTCTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGCAGCTATCAAGTTGATGACCTTATACTTAACTTTAACTTTAACTTTTAACTTTTAAAGTGTTCTTTTTAAGGGGTGTC  1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAGTTGTTGGTTG  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTAACTTTTTT  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC  1680  IR1'  
   |  |  |  | 1681 TAAGCGATTTCCGCCCTTTCGCTCGCTCGCTCGCTCGCACACTGCAACTTGTAA 1800   | 700 (000 (000 (000 (000 (000 (000 (000   |
|  | AGAAGCAGCTATCAAGTTGACTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC  1560 E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAGAGAGA  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  | IR1' 4IR2'4
   | IR1' 4IR2'4  | •  | IR1' 4IR2'4  | IR1' 4IR2'4  
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  | •  | 1501 TA 10001TTTTTTTTTTTTTTTTTTTTTTTTTTTTT  | •  | •  | •   
  | IR1' 4IR2'4   | IR1' 4IR2'4   | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4  
                 | IR1' 4IR2'4   | IR1' 4IR2'4   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  
  | IR1' 4IR2'4  | IR1' 4IR2'4  | IR1' 4IR2'4   |   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTTGACCTCTGGGTTAGCTTGGTTAATGTCCTATGGGTCGGC  1680  IR1'  | A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAGAGAGA  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTYGATGACCTTATACTTGATGGGCAATTTTACTATTACTATTTACTTTTTTTAAGGGGTGTC  1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAGTTGATTGA   | 2 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATGGATGAAAAAGGAAGAAGCAGCTATCAAGTTGATTGA   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | LET L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  LEDWENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAGAAGAGCAGCTATCAAGTTGATGACCTTATACTTTAACTTTAACTTTTACTATTAACTTTTCTTTTTT   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  
   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   
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   | ·  | ·  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCTTTGGTTGACCTCTGGGTAATGTCCTATGGGTCGGC 1680   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC 1680  | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATFTTTTTGGTCAAAAAGTTGTTGGTTGACCTCTGGCTTGGTTAATGTCCTATGGGTCGGC 1680   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTT  | ·   
   | ALVSD GIDK MEEAAIKLIDLILD GQF NLPFYY*  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGGTGGAATCGATAAAACGAAGAAGCAGCTGTCAAGTTGATTGA   | * Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGGGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGGGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTACAAGTTGATTGA   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGGGGTTICTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440 V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | ·  
   | 1561 TGAGGGTTTGCCCCGTAATCTTCCTGAAGTGCAGCATTGTCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGGTCGTTGGTTG  |  |  | TO 1   |  |
|  | AAAA TITOTATITOTATITOTATATATATATATATATATATATA  |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  « Element D   | V V E T L D
P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  |  |  |  | 1221 CTSCTSCSSSCTTTSCAPPPPTTACACPCCTTTAAACCPCCTTTCTATTCTTTTCCCCSSCSTACACCCCCAAASTTCASSCSTSCATTACCTAATACCCTTTAAASTT 1440  |  
   |   |   |   |  | E L O E N L K U I L K A A I P S I G P I K E Y P E U H Y Y M H L N D D D A L S A  | E LUEN L ROTIRA ATF STGFTKE V FEDH V Y M H L N D D D A L S A  | EIDEN LROTIRAATFSTGFTKEV FEDH VYM H LNDDDALSA  | EIDEN LROTIRAAT FST GFT KEVFEDH VYM H LNDDDALSA  
   | EIDEN LROTIRAAT FST GFT KEV FEDH VYM HLNDDDALSA  | EIDEN LROTIRAATFSTGFTKEV FEDH VYM HL N D D D ALSA  | EIDEN LROTIRAAT FST GFT KEV FEDH VYMHL NDDDALSA   |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | Lebent D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAGGAGCAGCTATGCCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   |
|  | AAAGACACTITICTATICTTTTGGGGGAGGATACCAGCTTGGGAGGGGGGGGAAATTTCGAAGGATACATTACCTAATATGCCTTTTAAAATT 1440   |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  « Element D   | V V E T L D
P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGGCAATTTAACTTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   
  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  • Element D   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATCTATACTTTATCTTTAACTTTTTCTATTTAACTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCTATTAACTTTTTTTT   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I   
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  |  |  |  | 1321 CTBCTBCBBCTTTACACCCCATTACACCCATTAAACCCCCTTTCTTT   |  
   |   |   |   |  | C J D C M L K Q I J K A A I F S I B F I K E V F E U M V Y M H L N D D D A L S A  | E LUEN LR QTIRA ATFSTGFTKE V FEDH Y Y M H L N D D D A L S A   | E I DEN LR QTIRA ATFST GFT KEV FEDH V Y M H L N D D D A L S A  | EIDEN LROTIRA ATFSTGFTKE V FEDH V Y M H L N D D D A L S A  
   | EIDEN LROTIRA ATFSTGFTKE V FEDH V Y M H L N D D D A L S A  | EIDEN LROTIRA ATFST GFT KEV FEDH V Y M H L N D D D A L S A   | EIDENLROTIRAATFSTGFTKEVFEDHVYMHLNDDDALSA  |  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N H A F K I  
   | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  - Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | V V E T L D P L E G L K A V S I L L G K I P A S E A E N F K D T L R N M A F K I  4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGAGCAATTTAACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | Lebent D  1441 GCCCTTGTTTCTGATGGGATCGATAAAAGGAGCAGCTATGCCTTTTCAAGACAATTTTTTTGGTCAAAAAGTTGTTGGTTG   |
|  |  | THE FLUITE COLKANDILL CALIFABERT RUILK MINAPRI   |   | ← Element D  | 4 Element D
1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  
   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   
  | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTTT   | ◆ Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTCTTTTTT   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTTT   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 4 Element D 1441 GCCCTTGTTTCT6ATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTT  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   
   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT  | • Element D  | - Element D  
  | • Element D  | • Element D  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTCACTATTAACTTTTTTTT  | 4 Element D 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTTACTATTAACTTTTTTTT   |  
  |  | THE ILUPECULARY SILLUNITAS EARTRUILKAAPRI  | THE ILUPLE OF ENTRY SIFE ON INTERFERENCE OF THE TRY I  |  |  | 1321 STAISTAISAAAACTTTRIGACECETTABAGGGGTTABAGGCGGTTCTATTCTTTTGGGGAAGATTCAGAAGCCGAAAATTTCAAAAATTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  
  | 1321 GTAGTAGAAACTTTAGACCCCCTTAGAGGGGATTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCCTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGGTTAAAGGCGGTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGGTTAAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | ·  | ·  | ·   | ·  | ·   
  |  | ·  | ·   |  | ← Element D  | 4 Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTTTTAAGGGGTGTC 1560   
   | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | • Element D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATACAGTTGATGACCTTATACTTGATGGGCAATTTAACTTTACCATTTTACTATTAACTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | LETEMENT D  1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGATTGA  |
|  |  |  |   |  | 1441
GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCATTTTACTATCACTTATCATTTTAAAGTTTAACTTTTCTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCATTTTACTATCACTTATCATTTTAAAGTTTAACTTTTCTTTTTAAAGGGGGTC 1560   
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACTTGATGGCCAATTTAACTTACCATTATCATATTAACTTTACTTTTTAAAGGGGGTC 1560  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  
   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCTTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCATTTTTTTT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCATTTTTTTT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCATTTTTTTT  
  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCATTTTTTTT   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATGGATAAAAGGAAGGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTATTCATTTTTTTT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   
  | 1441 GCCCTTGTTTCTGATGGAATGGATAAAAGGAAGGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTTCACTTTTACTATTAACTTTTCTTTTTTAAGGGGTGTC 1560  A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCATTTTACTATCACTTATCATTTTAAAGTTTAACTTTTCTTTTTAAAGGGGGTC 1560   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  
   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   |  |  
  |  |  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGATTGA   | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGCAGCTATCAAGTTGACCTTATACTTTGATGGGCAATTTAACTTTCTATTAACTTTTCTTTTTAAGGGGTGTC 1560   | ◆ Element D  
  |  |  |  |  | THE ILB FLEW LANDS SELWAL FROM ENTRU (LKH HAFRI  |   
  |   |   |   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   
  | 1321 GTAGTAGAAACTTTAGACCCCTTAGAGGGGTTTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTTTAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440   | 1321 GTAGTAGAACTITAGACCCCTTAGAGGGATTAAAGGCGGTTTCTATTCTTTTGGGGAAGATACCAGCTTCAGAAGCCGAAAATTTCAAAGATACATTACGTAATATGGCTTTTAAAATT 1440  |   
  | 1441 GCCCTTGTTTCTGATGGATCGATAAAACGAAGAAGCAGCTATCAAGTTGACTTAACTTGACGTGACATTTTACCTTACCTATCTAT  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGAAGCAGCTATCAAGTTGACCTTATACTTGATGGGCAATTTAACTTACCATTTTACTATTAACTTTTCTTTTTAAGGGGTGTC 1560 A L V S D G I D K N E E A A I K L I D L I L D G Q F N L P F Y Y *  | 1441 GCCCTTGTTTCTGATGGAATCGATAAAACGAAGCAGCTATCAAGTTGATCTTGATGGCCAATTTAACTTTCACATTTTAACTTTCTTT  |

2161	TATCGGGCTATCGGAATGGTAAGCCATCCGGCTGAGTTTGGAAGTGAACTTGAAGGAGATATAAATAGTATACTTGACTCGGTCGTTGATGAATCTGGTTTAAAAAGAAGAGGAGTTGAAA Y R A I G M V S H P A E F G S E L E G D I N S I L D S V V D E S G L K R R E L K	2280
2281	TGGAATAAAATAGACATATTCCGGYGYAGAGCATATGAGAAGAYTGTAGACTACTTTTTAGAACTCAGTAACCTTGGTAATCCACCAGTTCGTGTGGATATCTTACGGTGGGACATTGAA W N K I D I F R C R A Y E K I V D Y F L E L S N L G N P P V R V D I L R W D I E	2400
2401	GACAGCCGTCACAGTATACAAGGGCGGGATGATAACCAAAACCTGCAGAGGATGTACTATCTAT	2520
2521	GATGAAACAGGTICAGTAGATTGGGAGGAAGTGGCGTICTICTTGGATATTGGTGGTTCAAAGGTAGACCTAAAGGAACAGTTTAATAACTAAGTATTAATGAAGTTGATTCCAAGGAT D E T G S V D W E E V A F F L D I G G S K V D L K E Q F N I L S I N E V D S K D	2640
2641	AATGTACTAGTICAAGTGGCTGACTTTTTCGCGGGACTCAGTGTTTTTTCTAAGGAGAAGATTTGGGCTTTATGTAGACTGGAACTACGAAGAATGTGGACAAGAATTAGTTCCTGTA N V L V Q V A D F F A G L S V F S K E K F G L Y V D W N Y E E C G Q Q R L V P V	2760
2761	GAAAACGTTGAGTTCTCCAAAAAGGATAGGAAGCGTTTTGAAATTCTTTCT	2880
2881	CCTAAACCTGCTAACAGTATAAATTTCTGGCATTATGAACCCCAGAGTGATGCCGACAAAGGCACCTATAAGGTAACCTCAAATAGTTGTTTTTTAACTTGTTCTTTGGGGTGAGGGATTCA PKPANSINFNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3000
3001	CCCTCCCCCAAACCCCCACCCGAAGGCCCCGGCCTCGCTACGCTCGCT	3120
	TCGCTTCGCTCACATCTCTGAAATTCCTAAAACAGCCGCTTTCGCTGCGTTACTCAGATTGGGCGGGAAAAACCAGTGAATGAGATTGGCGGGCG	3240 3360
3361	(Insertion element A [FR-I] in pFVI) *******  GTTTAATGACATGITTAATGCATTTITCAGGITTTTAGAATGITAAATTATGGCGGCIGFCTICGGTTGTAACCGCACCCCATGAGAYITTAATATGAAAAAATTAAATAATATTATTAT  ORF3' M K K L N N I I M	3480
3481	GATATTAATAATGCACAGGTACTTCTTACGGGTGATGAACTTGAGGCAGAAAGTTATTGAGGCCCTAGAAGAAGGGAAGAGTGTTGCGATTAAGTACCAGGATGTAAGGGATTACCTCGA  I L I N H R Y F L R V N H L R Q K V I E A L E E G K S V A I K Y Q D V R D Y L D	3600
3601	CCTGAAAACAGGTCATAGGGTTATATTCCTTGAACACATTAACCCTGCAAAGGAGACCGCCGCTGAAATATTGGCTGACCTTGGCAACCTTGCAAAAAGCACTATATACAGCAAGTATAC L K T G H R V I F L E H I N P A K E T A A E I L A D L G N L A K S T I Y S K Y I	3720
3721	AACGAATGAGATTGTCAGGGACATCAAGAAGAGGTCGAAGAACAGGAATGTCCTCCTGGTGTTCAATGACTTTCAGTTGCTTTCTAAGAACACTGCAAGGGTTCTTTTGGATCTCATGGA T N E I V R D I K K R S K N R N V L L V F N D F Q L L S K N T A R V L L D L M E	3840
3841	AGATGTCCAAGTTCTTTGTAGTATCAGGGGCAGACCCCAGAAGGGTCAGGGGCGTTTGCTTAAGAATGACCATCCTAAGCGATAGGTCTGACGAGGTCACTGATATTAAGATACCCCT D V Q V L C S I R G R P Q K G Q G R L L K R M T I L S D R S D E V T D I K I P L	3960
3961	CATAGTCTTTGCGAGCTTTATAGCAATATTAACCTTTGTTAAGGCGGGCTCGGCTATCTAT	4080
4081	GGGGAGGACTCTTTTATGGAFTTCTTAAGTTCAGGCAGGTGCCTCCTGTTTATCTTCTGGGTCGGCCTTCGGCGGGGCTTATTACATTFTCTGGCTTTACGCCGCAGGTTATCAGTAAGT  G R T L L W I S *	4200
4201	CGGTGGGGGTCGTGGTAATTTGAAATGGTATACGCACGCCCTATTTTCGGTCTTTGTGGGGGTATTCTTTGGTTATCTCCTSAACGCAGATCTTTCACCATACTTTTTATGTTGACAAT  CRF4' M Y Y A R P I F G L C G G I L N L S P E R R S F T I L F Y V D N	4320
4321	TCTTTCATCTGTAGTGGTCGACTTTGCAGAAAAGGCGGCGTTAACGAGCACAAAAAGGCAACTTCACAATGTTTTCACCCTGATACCCTTTGTTCTCTTGTACCTCTTTTATGATGTGACC SFICSGRLCRKGGGVNEHKRQLHNVFTLIPFVLLYLFYDVT	4440
4441	ACAGGCGCCCCATGTTGTCGGGCGTATCTTCCCCATATTTTGCTTGATTCATGACTCCAACGGGCTGCCCCTTTTTTTT	4560
4561	AAGGGTAGTGGTCCCAGGGAAAAAAGGGCGTTAACAACTATAGGTATTCTTGCAGCGATTCTACTCCTTGTTATCTATGCGCCGATTTGCGCCGACTTCGGCGATTTCCCAGTGG K G S 6 P R E K R A L T T I G I L A A I L L L V I Y A P S P F A P T S A I S Q W	4680
4681	FR-II >  AGGGTTCTGGCAGCGGGGCCTCAAACAACAGCACCATAAATGTGAATTTTAACTTCAGAGGCAACGGTGACACCTGGATTCACCCTAATGGCAGTATCTTCATTGACTAT  K G S G S G A S N N R T D I N V N F N F R G N G D T W I H P Y P N G S I F I D Y	4800
4801	GTGAGCGACGGTGACAGCAGGGGTTTACAGGTACAGGGGTATCAGCCGGGGGAGGGCAGGGAAAGCACCTGAAATTGGATTCTAACACCACCGAAAACAAAC	4920
4921	GGGGGATGACTCTGGCAAGGCGGAGCCCTGCTTTTGAGAAGGTATGCAGTTTTATAGAGAAGTCTGAGAGGTTCTGTACTGACAAGAAAATCTATACTCAGAAGGTTTACCTGGACACCA G G *	5040
	GGACCGCCTGTAAGCTTGAGATTATCAGCTATATCGAGTCAAAGTCAAAAGTGAACTTTCGAGGGAGG	5160 5280

5281	GAGGTGGAAAAATGCATAGGAACACTTCTGCTTGCAGCGCTGCTGCAGTTTTTATACTGGCAGGTFCATCGGCTGCGGCAGATGTGGGTGTTGAACTCGATAAGAACAACACGA ORF5' N R N G T L L A A L L A V F I L A G S S A A A D V G V E L D K N N T	5400
5401	AGCCAGTGTATAACTCGACCCTTAGGGTTAAGGTCATAGCGAAGGCAGGC	5520
5521	CAGCICAGGGCTACTATGACCTCGAAACAGGTACCTGGGAAATAGGTGATATTCCCGCCTATGAGGAGAGGTCCCTGACACTTGTGTGCCTCCTCAACAGGACTGGGAATGTGACGGTGA 1 A Q G Y Y D L E T G T W E I G D I P A Y E E R S L T L V C 1. L N R T G N V T V	5640
5641	CCGCCAACGTGACTGCAGATGGTGATGAGAACCCTGCCAACAACAATGCCCAGTTGAAGTTCAGGGTCAGGGGGATCGCGGACCTTGAACTCAATGTGACCAGCAGTAAACAGAGTGCCA T A N V T A D G D E N P A N N N A Q L K F R V R G I A D L E L N V T S S K Q S A	5760
5761	GGCTTGGTGATACGGTCACATTCAATGTGAAACTCAAGAACAGGGGGCCCCCACGCTGCAAATAACATCAACGTTGCCAACTTCTCTCAGGAGGCCTTGCGATTCAGAGTTACAGTTACAR L G D T V T F N V K L K N R G P H A A N N I N V A N F F S G G L A I Q S Y S Y	5880
5881	CTACAGGTTACTTTGACGATGTGGCGAGGGAGTCGTTGAGACCCTTGATACCGGTGAGGAGGCCACACTTACAGTTGTGTGCCTTGTTAACAGGACAGGTGATCTCTCTGACTATG T T G Y F D D V A R E W I L E T L D T G E E A T L T V V C L V N R T G D L S D Y	6000
6001	TTTCAGTGCGTGAGGTGAATGAGGGATGATGTCTACAACAACATAGCCCGGGCCTCAGTCGCTGTTAAGGGAACTGACCTGGACCTTGACCTCTCTGTGAGTAAACCGAGGGCCT V S V R E V D E G D V N V Y N N I A R A S V A V K G T D L D L S V S K P R A	6120
6121	ATCAGGGTGACGTTGTCAATGTGGTCTGCCGTGTTAAGAACAATGGCCCTGAGGCCGCCCAGAATGCCAGGGTCAACCTGCAGCTACCTGCAGCTCCAGGATCGCAGGTCCAGAATGTGCAGGTGG Y Q G D V N V V C R V K N N G P E A A Q N A R V N L Q Ł P A N L Q V Q N V Q V	6240
6241	ACAGGGGCACCTACAGTAACGGTGTCTGGGTCATCGGTGACCTTGCAGACAACGAAGCAGCACCTCCTCAATATAACAGCAAGGGTTGTATCAGCGGGCAACTTCACAGTGAACGCCACGG D R G T Y S N G V W V I G D L A D N E A A L L N I T A R V V S A G N F T V N A T	6360
6361	CGGTTTCACCTGCAATCGACGACACCCCGTGAACAACGACGATACAGCGCTGGTATCTGCAGCGATACCTAAGAAGGCCCTCAAGGTGAGGATAAAGAACAACTCTGCGGTGACCA A V S P A I D D S N P V N N D D T A L V S A A I P K K A L K V R I K N N S A V T	6480
6481	TCAGGGTGCTCTTATATGTGAACATCAACGGCAAAATCACCAGGAAGACCTACAACTTCTACCTGAAGAATGGCCTCAGCAGGGACCTCAGCCTTGGATACTTCCAGCTCGGCA I R V L L Y V N I N D H G K I T R K T Y N F Y L K N G L S R D L S L G Y F Q L G	6600
6601	CCAGTGCGCTCTTCAAGCAGTACACCTACAACACCAATTACAGGCCAAGGACAGTATCCTACGAGAACACCTACAATGCCACAGCGTCATAACCCAAAGGGTCAACGTGTCTGGGGTCA T S A L F K Q Y T Y N T N Y R P R T Y S Y E N T Y N A T S Y I T Q R V N Y S G V	6720
6721	AAGGAAGGCAGAAGGCACCTGTTGTTAGGATTGCAACACTGCTGCTTGATGAAAACGGCACATCACTACAATAAATCTACAATACATTTTTAATTTTTT	6840
5841	ATGATGCCCCAATAAGGAAACTCTCCAATCAAATCTATGAGGCGATAGTCGTBATGAGGCAGATAGCTGAAATGAGGAAGGAGGTTTCGCAGCATGGGTTTGATGTCAGGATGATGAAG ORF6' M R Q I A E M R K E V S Q H G F D V R M M E	6960
5961	TCCCTGGCATGAAGGTTGCTATCGCAGGGGACGGGAAGTCAACTACCTTTTCATGTTACTCCCCTTTAGGGACAAGTTTAAACTAAAAAAGCGAGATGTCTGGTTGTTCAAGAAACTTT V P G M K V A I A G D G E V N Y L F H L L P F R D K F K L K K R D V W L F K K L	7080
7081	CCTATAAATTCCAGGCACGGCCTTTCATGGTAACCTTTGACAAGATGCTATCCTTCTACCCACTACACGCCCCTTGAAGAAGCTGGCGAGCACTTTGAACTCGATATAAGGAATTCAAGGG S Y K F Q A R P F M V T F D K M L S F Y P L H A L E E A G E H F E L D I R N S R	7200
7201	FR-II  GCCTGATGTTTTCTTTTGATACCATTGTGTCAGAGCAGTTGCAGCAACGGCTTGTTGTGTAGCCGCCAAAAACGCCTAGAGGGTAACCCCAGCAGGTGTTTCCTTTTTTTT	7320
7321	GTTTATTTGTFCAACTCGTAACCTGCAAAAGCCATGTGAACAACACCAGGTCCCCACCTTCAAAAACAGACAAAATTTTCAATGAATG	7440
7441	Element E > TTTTGGGGTTCCAGCACACTATTCTTTATGCAATGCTATAACGAATGAAT	7560
561	TCAGGTTAGATTTTAAAGATGAATTAAAGAAGAAGATAACCGGTAAAGAAGTAGAATTTCCCAAGTATACAACCCAAATTATAAATTTAGCAAATCAAAACGCGCAGGGTACCCGACCAAGGG I R L L L R L L R L L R L L R L L R L L L R L L L R L L L R L L R L L R L L R L L R L L R L L R L L R	7680
681	TAGTAGGTCAGATGTCAGATTGATACATGAATGCCCCGACAAGAGTTACGAAGGTTGGAAAAATGGTATCTGGAACATTATTCTGACCGCATCGAAAAAGCAACAAAAAGATCAGCA V V G Q N S O L I H E C P D K S Y E G W K K W Y L E H Y S D R I E K A T K K I S	7800
801	AAATGATAGAAAATATGAAAGCTGCTATGGAATTGATAGATGAAGAAATGATCAGGAAATGGTAGAAGATTTAGTTATAACCAAAACAGCGGAAGGTCTAATAATTCAAGAAATCATTC K M I E N M K A A M E L I D E E M I R K W V E D L V I T K T A E G L I I Q E I I	7920
921	TGAAAACTATCGCTGAAGAAGCAGGTCTGGAGTGGCGCTTAGCAACCTCAAAAGAGGAAAGTAAAAACATTGATGGATCTACACCGGTTTCCATAAAGCCCATGAGTTATG L K T I A E E A G L E W R L A T S K E E S K N I D G F I G S T P V S I K P M S Y	8040
041	* I N L K S Q R AATCAATGCGACCCACGGTAAGGGAGGAAATAGACATACAGACAATTTTTTACAAAAAGCCTAAAAATAGCAGATATCTTTATATCTATC	8160

8161	EKKPNVEQYFFEFENNKIKKYTRPYYLRIDQEQRTTVKFK	8280
8281	Y N E S Y Y K G N K E R I F E I H D N I R R N V I E N S L K L T E N I R S E I L TAGENTATATATATATATATATATATATATATATATATATATA	8400
8401	D K F N H D L E Y G I S N R G A C A A A I M T T G T G L F P D L V W D G M I S Y ICTITIGAAATTGTGGTCTAATTCATAACCTATTGAATTCTTCCTGCGCATGCAGCAGCAATCATGGTGGTTCCAGTGCCAAGAAAGGATCAAGAACCCAATCACCCATGATCGAATAC	8520
8521	M N I L R Y A L E F P Y A A A R K R L N K H N L R Q S V G T L D T W V D S F W Q ATGITTATACCCTATACGCAAGTCAAGGGGTGCGCTCTTTTCTTAAATTTTATGATTTATGTCTTTGGAAACTCCTGTTAAGTCAGCAAACAACAACAACAACAACAACAACAACAACAACAA	8640
8641	N R E E W F Y A S E R R L K R E E E T K F Q R P G E K R F I L I Y E H E H T V Y TTGCGTTCTTCCCAAAAATAAGCGCTTTCCCTGCGCAATTTTCTTTC	8760
8761	A N P P L M G S G M F K T P K N S Q K R W I I F P L V Q Y G R D F F F D I T R V GCATTCGGAGGAAGCATTCCAGACCTTGATTGTTTGGTTTGTTT	8880
8881	H M P Y L Q F K K G I K R T A D G I M I I Y Y G G P A T Y R D Y E H M Y K E L E TGGTTAGGGTATAATTGAAACTYYTTACEAATTTTCCTTGTAGCATCCCTTATTAATGATCACCACCCCCCAGGTGCAGTTACCCTGTCGACTTCATGCCATACCTTTTCCAATTCT	9000
9001	E H N L N Y S R L G D E E D 1 L T E E I K P N L E S F L R D W I E V N P Y P P S TCATGCATTAAATTATAAGACCTCAATCCATCTTCTCATCTATCAGAGTTTCTTCAATTTTAAGGTTCAGAAAAAAGGGGGGTCCCATATTTCAACCATAGGATACGGAGGAGAC	9120
9121	T V V L N I S K D K L E N M D A S N K F Y I R H T T K M MERZEM GTGACAACAAGATTAATGCTTTYATCTTTCAATTCATCATCAGCAGAATTTTTAAAATAGATTCTATGTGTAGTTTTCATGGTTCCCTCTTTTTATTTTTTTT	9240
9241	TTAGTGTGGAAATCCTTTCAAGAGAGTATAAATCAGATTATTATAATGAATG	9360
9361 9481 9601	- Element E  ACTITATTITATTATACAGTAGAATAAAATATTATAATATTITCTATTGGATACTATIAATTATATTGTATAAGTTAATAGTATACTATAGAAGTATCTTGAAGTAGAATAAAAG TGCTATACTCGCAAA4ACAAAAGAAAAAAACAAGGAATACAAGACCGTTCAGCATATAAAAGTITAAAAGGTTAAAAGGAATACAAAGGCAAAACCAAAAGCAAAAACAAAAAAACCTGATTTAAATTACTAAGAGAAAAATCTGGAAAAAATATGAAAAAACCTGATTTAAAATTACTAAGAGAACATCTTGGAAAAAATATGACAATGAACTTCAAAAGAAAAAACCGGATTCAAATGAAATTACAGAAAAACCTGATTTTAAATTACTAAGAGACATCTTGGAAAAAATATGACAATGAACTTCAAAAGAGAAAAAACCGGATTCAGATAGAATGAACTGCAAGTAGAATTCAATAAGCT  ORF7' M T M T J K E K T E L Q D Q I D E L Q V E F N K L	9480 9600 9720
9721	ACAAAACAAATATAAGCATATAAAATCTCTTCTAGACAAAAAGAGGAGGAGGAAGTTAACTACTTGGAGAACGAAGTCAAAAGACTTCAGAACAGGGGGATTATTGAGATATTGTTAGAAAA Q N K Y K H I K S L L D K K E R E V N Y L E N E V K R L Q N R G I I E I L L E K	9840
	Element F →	
9841	ACTTAGAAAGAAAAAAAGCCATTGAAGGGGAAGTTGAATACAGCAGGTAGTGGTTCTCTTGTTGTCAATGTCGTCTAAACCATTAACTGATATCGTAGTTAAAGTATGCAAGGACAAGGAT	9960
	LRKKKA I EGEVEYSR*  ORF12 VVLLLSM SSKPLTDIVVK VCKDKD	
9961	SAAAAABATGAAAAAGAGCTCATAATAGAAAAGGATCTTGTTGTTCTATAAATATGGGTGCTGAAGGAACTGAATTGAACATCAAGGCTCCTAAAAGCAAAATAGATAAATTCATGCAA E K D E K E L I I E K D L V V S 1 N M G A E G T E L N I K A P K S K I D K F M Q	10080
10081	TTTTTTGCAGAAAATGAAAATAAAATGCTTCGCTTATCAGTAAAAACCAGTCAGGAAGATATTTTAGAATATTATAGTGGATCTACATACCTCCTTATAGAGGGACTTGGTGTTTTGGAG FFAENENKMLRLSVKTSQEDILEYYSGSTYLLIEGLGVLE	10200
10201	GGAGATCCAGCGAACTTAATTCTTTATTTGAATTATTTAT	10320
	AGAGTAAATTGCGAATTGTAACCAGAAACCAAGGTCCTGCTAACATGACCAACTACACTACACTAACCAAGACCAAGACCAAAACCGCAACCCTGTACTGTCATCTGTCAGAGAGAG	10440 10560
10561	TITACTACAGGTTCATGCCCTTGTCCCTGTTACAAGTAGAAATTCACTCTCTGTCTCCCGGGCAATGGGGTTGTTTTTTGTTACAAGTAGAAATTCACTCTCTGTCCCACCGTGGGCC	10680
10681	* M Y F Y P K S N Y L Q I A P L Q CATGTGCTTATATAGAAATTTGGTATTAATTCTTTTCAATTAGAAACATATATACAATAAGAAGTTTAGGATTAGAAATAAGGTTTCGAATTGTAAAGTTGTATTGCGGGGAGCT	10800
10801 <b>OR</b> F	L H K L L S R F K E F V P I D E A R Q K Y R V G Q L V P L F L H T S D A L V Q P GCAGATGTTTGAGAAGAGACCTAAACTTTTCAAAAACAGGGATGTCCTCAGCCCGTTGTTTGT	10920
10921	Y D E Y A G G W W Y Q Q N Y P G W S R P L G D R R L F H D Y F GTACATCCTCGACGGCCCCCCCCCCCCCCCCCCTCACCTTGATTGTAGGGCCCCCCAGGATCTGGGAAGACCGTCACGACGAAGTATGTGATCAACGAA 11014	

10921 GTACATCCTCGACGGCGCCACCCCACCACCACCTGTTGATTGTAGGGCCCCCAGGATCTGGGAAGACCGTCACGAAGATATGTGATCAACGAA 11014
Y I L D G A T P P H L Ł I V G P P G S G K T V T T K Y V I N E

Complete nucleotide sequence of cFR-II from M.thermoformicicum CSM3 (EMBL accession number X69114; see also Chapter 6).

	EccRI cFR-II ►	
1	GAATTCACAAACCCAAGCCTCCATCTCAGGATCACCAAGACCCACAGAGGGACACCTGGGTCCACCCTTTCCCCAACGGCACTCACT	120
121	ACAGTYTATCACAGGTACTGCACTAAGCCGGGGCCGGAGCGTAAGGTTAGGTCCTCTGAGGGCCAGAGCAATGGGAGTACTGGAGAAAACGGTACGGGGTGATGTTCTGTCGGGATCTGA	240
241	TATCGATGATGTGGTGAGGTCATATCGAAGCTGGATTATGATCACGGCAAGAAGATATTCCTCCAGAGGGTTTACCTTGACCTCAACACTGCCTGTAAACTGCATATACTCAGCTTCAT	360
361	TGAGGAGAGGTCAGGAGTGACATCTCGCGGAGGGCTATYCAGATGATBATAGATGATTATGAGAGGGAATACGGGAACCTCATTAACCTTGTGAAGAGGGACATCCTCATGTGGATATA	480
481	GGGCCCTTGCAGCGGTTCCATCCCCATTTATTTTTTCTTATGTAACTTGTCCACTGATCAGCATCTCCATGGTTACATAAGAATGTACCCAAAGGCATGCTTTAAAGCCCCACCCGAGTT	600
601		720
721		840
	CORFS MIDGSAIKPTYNSTMKIKAIVKAGNODVONVTATVRL	
	COMPANY OF THE STREET OF THE S	
641	CTGAGGGCCTCGTACTCCAGGACTACTACATBAGCCAGGGATACTATGACCTCGAGACAGGTACCTGGGAGGTTGGTGACATCCCTGCCTATGAGGAGAGGTCCCTGACATTCGTTTGCC	960
041	PEGIVIDEN Y Y N S D G Y Y D L E T G T W E V G D I PA Y E E R S L T F V C	300
	PEGLY LUDITHS UNIT DE LA LWEY NO 1 PATECAS LIFT	
061	TECTGAACAGGACTGECAGCATTACTGTGAACGCCAGTGTAACAGCTGATGGGGATGATAACAGTGCAAACAACAATGCAGAGTTAGGCTTCAAGGTGTTTGGTATATCAGACCTTCAGC	1080
901		toon
	LLHRTGSITV KASVTAD GODNSANN HAELGFKV FGISDLQ	
	·	
081	TTAACGTCACGAGCAATAAACAGACCCCACGGCTCGGCGAAACTGTGAGACTGACGGTTAAAACTTAAAAACATGGCCCCCATGACGCGAACAATGTCAAGGTAAGGTAACTTCCTCTCAG	1200
	LNYTSNKQTPRLGETVRLTVKLKNNGPHDANNVKVGNFLS	
201	GCGGACTCGTCGTGCAGAGTTTCAGCTATGATGCCGGCTACTTCGATGACCTACAAAGGAGTGGGTCTTTGACACCCTTGCAGCGAGTGAAGAGGCGACCCTCACACTTGATTGCCTTG	1320
	G G L V V Q S F S Y D A G Y F D D L T K E N V F D T L A A S E E A T L T L D C L	
321	TCAACAGGACAGGTGAACTCTCAGACTATGTTTCAGTAAGGGAGGTCGATGAGGGCGACACACAC	1440
	V N R T G E L S D Y Y S Y R E Y D E G D T N Y Y N N M A R A T L S Y R G T D L D	
441	TCGACGTTTCAGCGAGTAAGACAAGGGCCTATCAGGGTGATGTGATCAATGTTATCTGCCGCGTGAAGAACAATGGCCCTGAGAATGCCCAGAACGTGATTGTCAACCTGCAGCTACCCG	1560
	L D V S A S K T R A Y Q G D V I N V I C R V K N N G P E N A Q N V I V N L Q L P	
	•	
561	TGAACCTACAGGTCCAGAACGTCCAGGTGGACAGGGGTACTTACAGTAACGGCAACTGGTCCATCGGTGATCTTGCAGACAATGAAACAGCGCTTCTCAACATCACTGCAAGGATTGTGT	1680
	V N L O V O N V O V D R G T Y S N G N W S I G D L A D N E T A L L N I T A R I V	
182	CTGCAGGTAACTTCACAGTGAACGCCTCTGCAGTCTCATCTGCAGTTGATCACAGTAACTCCGTGAACAACGATGATACAGCGATGATATCTGCAGCAGTCCCCAAGAGGGCCCTCAAAC	1800
001	S A G N F T V N A S A V S S A V D D S N S V N N D D T A N I S A A V P K R A L K	1500
	3 M G R F I W M S M W S S M W D D S R S Y R R D D I M N I S M M Y F K K M L K	
401	TCAAGATAAAGAACACTCTGCAGTGACGATCAGAGTACTCCTATATGTTACAGTCAATGATCACGACAAAATCACCAGGAAGACCTACAACTTCTACCTCAAGAAGGGCCTGAGCAGAG	1920
001	LKIKNNSAVTI RVLLYVTVNO HOKITRACHOMOMOMOMOMOMOMOMOMOMOMOMOMOMOMOMOMOMOM	1920
	CK TK W & 2 M & 1 TK & C C L & 1 A M D & D K T 1 K K 1 L M L 1 CK K G C 2 K	
		***
921	AACTCAACCTTGGGTACTTCCAGATCGGTACAAGCGCCCTCTTCAAGCAGTACACCTACAACACCACACTACAAGGTCAAGGACAGTGGCCTATGAGAACATCTACAACTCCACCGGTGTCA	2040
	ELM LGYF QIGTSALFK QYTYNTNYR SRTVAYENIYN STGV	
041	GGACACAGAGGGTGAGCGTCAGTGGTGTGAAAGGAAGGCAGAAGGCCCTGTGGTGAGGCTAACACCTTAACGTTCGACGAAAACGGTTCAAACATACAATAAACAACTTTCAATTTAT	2160
	RT Q R V S V S G V K G R Q K A P V V R L T T L T F D E N G S N I Q *	
	TTTTTTGGGAGGTAAATTATGGATATAGAAGATGCTAAAAAGATGGCTTCCCTGCTGGAAATTAAAAATGAGCTAAAGGAATATGATTTTGAAATGAGGATCTAAAGGATCAAAGGAT	2280
	ATTECAATAGCTGGAGATGGTGAAACGACATATCTATTCATAATGTTATTGCCTTACAGGAAGATTCAGTATACGTAAAAGACATGTCTGGAAGTTCAGACCCTTGCCTATAAGTTT	2400
401	AAGGCAAACCATACATTYTGACCTACAATATCATGACAACGATATATCCTTTACATGCACTTAATGACGCAGGTGATCATTTCGAATGGATGTTGAAAAGGCGAAGGGATTAATGTTCTC	2520
	◆ cFR-II	
521	######################################	2640
641	YTAGTGATCAAAGGTTTTGATCACAAATCAAA	2675

## Curriculum vitae

The author of the present thesis was borne in December, 1960, in Clausthal-Zellerfeld, Germany. After having completed the Albert-Schweitzer Gymnasium in Alsfeld, Germany, he started in 1980 the study of biology at the Philipps-University of Marburg, Germany. The graduation in the disciplines of molecular genetics (Prof. Klein), microbiology (Prof. Thauer), biochemistry (Prof. Kindl) and botany (Prof. Henssen) in 1985 was followed by a 'Diplomarbeit' at the lab of Prof. Klein and Prof. Thauer, which was finished in November 1986. In January 1988 he started as a Ph.D. student at the Department of Microbiology, Bacterial Genetics Group, Wageningen Agricultural University, The Netherlands.

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